



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Suzuki, Shintaro
- (ii) TITLE OF INVENTION: Protocadherin Materials and Methods
- (iii) NUMBER OF SEQUENCES: 115
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & Borun
 - (B) STREET: 233 South Wacker, 6300 Sears Tower
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 18 JUN 1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/263,161
 - (B) FILING DATE: 27 JUN 1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Greta E. Noland
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 - (C) REFERENCE/DOCKET NUMBER: 27866/34703
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 - (A) TELEPHONE: 312/474-6300
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 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AARSSNNTNG AYTRYGA

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTRCTRTTTC GNGGNNN

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGGGAGTGG ACTTTGAGGA GCAGCCTGAG CTTAGTCTCA TCCTCACGGC TTTGGATGGA 60
GGGACTCCAT CCAGGTCTGG GACTGCATTG GTTCAAGTGG AAGTCATAGA TGCCAATGAC 120
AACGCACCGT A 131

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Gly Val Asp Phe Glu Glu Gln Pro Glu Leu Ser Leu Ile Leu Thr
1 5 10 15
Ala Leu Asp Gly Gly Thr Pro Ser Arg Ser Gly Thr Ala Leu Val Gln
20 25 30
Val Glu Val Ile Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAACGCATGG	ATTTTCGAGGA	GTCTTCCTCC	TACCAGATCT	ATGTGCAAGC	TACTGACCGG	60
GGACCAGTAC	CCATGGCGGG	TCATTGCAAG	GTGTTGGTGG	ACATTATAGA	TGTGAACGAC	120
AACGCACCTA	A					131

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Ala Met Asp Phe Glu Glu Ser Ser Ser Tyr Gln Ile Tyr Val Gln
1 5 10 15

Ala Thr Asp Arg Gly Pro Val Pro Met Ala Gly His Cys Lys Val Leu
20 25 30

Val Asp Ile Ile Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCGACTGG	ACTTTGAGAC	CCTGCAGACC	TTCGAGTTCA	GCGTGGGTGC	CACAGACCAT	60
GGCTCCCCCT	CGCTCCGCAG	TCAGGCTCTG	GTGCGCGTGG	TGGTGCTGGA	CCACAATGAC	120
AATGCCCCCA	A					131

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Leu Asp Phe Glu Thr Leu Gln Thr Phe Glu Phe Ser Val Gly
1 5 10 15
Ala Thr Asp His Gly Ser Pro Ser Leu Arg Ser Gln Ala Leu Val Arg
20 25 30
Val Val Val Leu Asp His Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGGGCCTGG ATTACGAGGC ACTGCAGTCC TTCGAGTTCT ACGTGGGCGC TACAGATGGA 60
GGCTCACCCG CGCTCAGCAG CCAGACTCTG GTGCGGATGG TGGTGCTGGA TGACAACGAC 120
AACGCCCCCTA A 131

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Gly Leu Asp Tyr Glu Ala Leu Gln Ser Phe Glu Phe Tyr Val Gly
1 5 10 15

Ala Thr Asp Gly Gly Ser Pro Ala Leu Ser Ser Gln Thr Leu Val Arg
20 25 30

Met Val Val Leu Asp Asp Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGGCGTTTG ATTTTGAGGA TCAGAGAGAG TTCCAGCTAA CCGCTCATAT AAACGACGGA 60
GGTACCCCGG TTTTGGCCAC CAACATCAGC GTGAACATAT TTGTTACTGA CCGCAATGAC 120
AACGCCCCGC A 131

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Ala Phe Asp Phe Glu Asp Gln Arg Glu Phe Gln Leu Thr Ala His
1 5 10 15
Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
20 25 30
Ile Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
AAGGCGGTGG ATTACGAAAT CACCAAGTCC TATGAGATAG ATGTTCAAGC CCAAGATCTG      60
GGTCCCAATT CTATTCCTGC TCATTGCAAA ATTATAATTA AGGTCGTGGA TGTCAACGAC      120
AACGCTCCCA A                                                                131
```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Lys Ala Val Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln
1           5           10           15
Ala Gln Asp Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile
          20           25           30
Ile Lys Val Val Asp Val Asn Asp Asn Ala Pro
          35           40
```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
TATGACCATG ATTACGAGAC AACCAAAGAA TATACACTGC GGATCCGGGC CCAGGATGGT      60
GGCCGGACTC CACTTTCCAA CGTCTCCGGT CTAGTAACCG TGCAGGTCCT AGACATCAAC      120
GACAA TGCCC CCCC                                                                135
```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Asp His Asp Tyr Glu Thr Thr Lys Glu Tyr Thr Leu Arg Ile Arg
 1 5 10 15
 Ala Gln Asp Gly Gly Arg Thr Pro Leu Ser Asn Val Ser Gly Leu Val
 20 25 30
 Thr Val Gln Val Leu Asp Ile Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGTCTGA TTACGAGGAG AACGGCATGT TAGAGATCGA CGTGCAGGCC AGAGACCTAG 60
 GACCTAACCC AATTCCAGCC CATTGCAAGG TCACAGTCAA GTCATCGAC CGCAATGATA 120
 ACGCCCCCA 129

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Gly Val Asp Tyr Glu Glu Asn Gly Met Leu Glu Ile Asp Val Gln
 1 5 10 15
 Ala Arg Asp Leu Gly Pro Asn Pro Ile Pro Ala His Cys Lys Val Thr
 20 25 30
 Val Lys Leu Ile Asp Arg Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
AAGGGGTTGG ACTACGAAGA CACCAAACTC CATGAGATTT ACATCCAGGC CAAAGACAAA      60
GGTGCCAATC CGGAAGGAGC GCATTGCAAA GTACTGGTAG AGGTTGTGGA CGTTAACGAC      120
AATGCCCCCTC A                                     131
```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Lys Gly Leu Asp Tyr Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln
 1           5           10           15
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu
 20          25          30
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro
 35          40
```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
AAGGGTTTGG ACTTTGAGCA AGTAGATGTC TACAAAATCC GCGTTGACGC GACGGACAAA      60
GGACACCCCTC CGATGGCAGG CCATTGCACT GTTTTAGTGA GGGTATTGGA TGAAAACGAC      120
AATGCGCCTC T                                     131
```


(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Gly Leu Asp Phe Glu Gln Val Asp Val Tyr Lys Ile Arg Val Asp
 1 5 10 15
Ala Thr Asp Lys Gly His Pro Pro Met Ala Gly His Cys Thr Val Leu
 20 25 30
Val Arg Val Leu Asp Glu Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAGGGTATAG ACTTCGAGCA GATCAAGGAC TTCAGCTTTC AAGTGGAAGC CCGGGACGCC 60
GGCAGTCCCC AGGCGCTGTC CGGCAACTGC ACTGTCAACA TCTTGATAGT GGATCAGAAC 120
GACAACGCCC CTAA 134

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Gly Ile Asp Phe Glu Gln Ile Lys Asp Phe Ser Phe Gln Val Glu
 1 5 10 15

Ala Arg Asp Ala Gly Ser Pro Gln Ala Leu Ala Gly Asn Thr Thr Val
 20 25 30

Asn Ile Leu Ile Val Asp Gln Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAGCCGTTTCG ACTATGAGCA AACCGCCAAC ACGCTGGCAC AGATTGACGC CGTGCTGGAA 60

AAACAGGGCA GCAATAAATC GAGCATTCTG GATGCCACCA TTTTCCTGGC CGATAAAAAC 120

GACAATGCGC CAGA 134

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Pro Phe Asp Tyr Glu Gln Thr Ala Asn Thr Leu Ala Gln Ile Asp
 1 5 10 15

Ala Val Leu Glu Lys Gln Gly Ser Asn Lys Ser Ser Ile Leu Asp Ala
 20 25 30

Thr Ile Phe Leu Ala Asp Lys Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCGGCTGG ATTTCGAACA GTTCCAGCAG CACAAGCTGC TCGTAAGGGC TGTTGATGGA 60
GGAATGCCGC CACTGAGCAG CGATGTGGTC GTCAGTGTGG ATGTCACCGA CCTCAACGAT 120
AACGCGCCCT A 131

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Lys Arg Leu Asp Phe Glu Gln Phe Gln Gln His Lys Leu Leu Val Arg
1 5 10 15
Ala Val Asp Gly Gly Met Pro Pro Leu Ser Ser Asp Val Val Val Thr
20 25 30
Val Asp Val Thr Asp Leu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGGGGATAG ACTTTGAGAG TGAGAATTAC TATGAATTTG ATGTGCGGGC TCGCGATGGG 60
GGTTCTCCAG CCATGGAGCA ACATTGCAGC CTTGAGTGG ATCTGCTGGA CGTAAATGAC 120
AACGCCCCAC T 131

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Ile Asp Phe Glu Ser Glu Asn Tyr Tyr Glu Phe Asp Val Arg
1 5 10 15
Ala Arg Asp Gly Gly Ser Pro Ala Met Glu Gln His Cys Ser Leu Arg
20 25 30
Val Asp Leu Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAGGCATTGG ACTTTGAGGC CCGGCGACTG TATTCGCTGA CAGTTCAGGC CACGGACCGA 60
GGCGTGCCCT CGCTCACCGG GCGTGCCGAA GCGCTTATCC AGCTGCTAGA TGTCAACGAC 120
AACGCACCCA T 131

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Ala Leu Asp Phe Glu Ala Arg Arg Leu Tyr Ser Leu Thr Val Gln
1 5 10 15
Ala Thr Asp Arg Gly Val Pro Ser Leu Thr Gly Arg Ala Glu Ala Leu
20 25 30
Ile Gln Leu Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
AAGCCAATTG ATTACGAGGC AACTCCATAC TATAACATGG AAATTGTAGC CACAGACAGC      60
GGAGGTCTTT CGGGAAAATG CACTGTGTCT ATACAGGTGG TGGATGTGAA CGACAACGCC      120
CCCAA                                             125
```

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Lys Pro Ile Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Met Glu Ile Val
1           5           10           15
Ala Thr Asp Ser Gly Gly Leu Ser Gly Lys Cys Thr Val Ser Ile Gln
                20           25           30
Val Val Asp Val Asn Asp Asn Ala Pro
          35           40
```

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
AAGCGGGTAG ACTTCGAAAT GTGCAAAGA TTTTACCTTG TGGTGAAGC TAAAGACGGA      60
GGCACCCAG CCCTCAGCAC GGCAGCCACT GTCAGCATCG ACCTCACAGA TGTGAATGAT      120
```

AACCCTCCTC GGTTCAGCCA AGATGTCTAC AGTGCTGTCA TCAGTGAGGA TGCCTTAGAG	180
GGGGACTCTG TCATTCTGCT GATAGCAGAA GATGTGGATA GCAAGCCTAA TGGACAGATT	240
CGGTTTTCCA TCGTGGGTGG AGATAGGGAC AATGAATTTG CTGTGATCC AATCTTGGGA	300
CTTGTAAG TTAAGAAGAA ACTGGACCGG GAGCGGGTGT CAGGATACTC CCTGCTCATC	360
CAGGCAGTAG ATAGTGGCAT TCCTGCAATG TCCTCAACGA CAACTGTCAA CATTGATATT	420
TCTGATGTGA ACGACAACGC CCCCCT	446

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys	Arg	Val	Asp	Phe	Glu	Met	Cys	Lys	Arg	Phe	Tyr	Leu	Val	Val	Glu	1	5	10	15
Ala	Lys	Asp	Gly	Gly	Thr	Pro	Ala	Leu	Ser	Thr	Ala	Ala	Thr	Val	Ser	20	25	30	
Ile	Asp	Leu	Thr	Asp	Val	Asn	Asp	Asn	Pro	Pro	Arg	Phe	Ser	Gln	Asp	35	40	45	
Val	Tyr	Asp	Ala	Val	Ile	Ser	Glu	Asp	Ala	Leu	Glu	Gly	Asp	Ser	Val	50	55	60	
Ile	Leu	Leu	Ile	Ala	Glu	Asp	Val	Asp	Ser	Lys	Pro	Asn	Gly	Gln	Ile	65	70	75	80
Arg	Phe	Ser	Ile	Val	Gly	Gly	Asp	Arg	Asp	Asn	Glu	Phe	Ala	Val	Asp	85	90	95	
Pro	Ile	Leu	Gly	Leu	Val	Lys	Val	Lys	Lys	Lys	Leu	Asp	Arg	Glu	Arg	100	105	110	
Val	Ser	Gly	Tyr	Ser	Leu	Leu	Ile	Gln	Ala	Val	Asp	Ser	Gly	Ile	Pro	115	120	125	
Ala	Met	Ser	Ser	Thr	Thr	Thr	Val	Asn	Ile	Asp	Ile	Ser	Asp	Val	Asn	130	135	140	
Asp	Asn	Ala	Pro	145															

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
AAGGGGGTTG ATTATGAGAC AAACCCACGG CTACGACTGG TGCTACAGGC AGAGAGTGGA      60
GGAGCCTTTG CTTTCTCGGT GCTGACCCTG ACCCTTCAAG ATGCCAATGA CAATGCTCCC      120
CGTTTCCTGC AGCCTCACTA CGTGGCTTTC CTGCCAGAGT CCCGACCCTT GGAAGGGCCC      180
CTGCTGCAGG TGGAAGCAGA CGACCTGGAT CAAGGCTCTG GAGGACAGAT CTCCTACAGT      240
CTGGCTGCAT CCCAGCCAGC ACGGGGCTTG TTCCATGTAG ACCCAGCCAC AGGCACTATC      300
ACTACCACAG CCATCCTGGA CCGGGAAATC TGGGCTGAAA CACGGCTGGT ACTGATGGCC      360
ACAGACAGAG GAAGCCCAGC ATTGGTGGGC TCAGCTACCC TGACAGTGAT GGTCATCGAT      420
ACCAACGACA ATGCTCCCCT                                440
```

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Lys Gly Val Asp Tyr Glu Thr Asn Pro Arg Leu Arg Leu Val Leu Gln
1           5           10           15
Ala Glu Ser Gly Gly Ala Phe Ala Phe Ser Val Leu Thr Leu Thr Leu
20          25          30
Gln Asp Ala Asn Asp Asn Ala Pro Arg Phe Leu Gln Pro His Tyr Val
35          40          45
Ala Phe Leu Pro Glu Ser Arg Pro Leu Glu Gly Pro Leu Leu Gln Val
50          55          60
Glu Ala Asn Asp Leu Asp Gln Gly Ser Gly Gly Gln Ile Ser Tyr Ser
65          70          75          80
Leu Ala Ala Ser Gln Pro Ala Arg Gly Leu Phe His Val Asp Pro Ala
85          90          95
```

Thr Gly Thr Ile Thr Thr Thr Ala Ile Leu Asp Arg Glu Ile Trp Ala
 100 105 110
 Glu Thr Arg Leu Val Leu Met Ala Thr Asp Arg Gly Ser Pro Ala Leu
 115 120 125
 Val Gly Ser Ala Thr Leu Thr Val Met Val Ile Asp Thr Asn Asp Asn
 130 135 140
 Ala Pro
 145

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAGGTCTCGA TTATGAGGCA ACTCCATATT ATAACGTGGA AATTGTAGCC ACAGATGGTG 60
 GGGGCCTTTC AGGAAAATGC ACTGTGGCTA TAGAAGTGGT GGATGTGAAC GACGGCGCTC 120
 CAAT 124

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Gly Leu Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Val Glu Ile Val
 1 5 10 15
 Ala Thr Asp Gly Gly Ala Phe Asp Glu Asn Cys Thr Val Ala Ile Glu
 20 25 30
 Val Val Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Asp Xaa Asn Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Xaa Asp Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Xaa Asn Asp Asn Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AAGCGGATGG ATTTTGAAGA CACCAAACCTC CATGAGATTT ACATCCAGGC CAAAGACAAA 60
GGTGCCAATC CCGAAGGAGC GCATTGCAAA GTACTTGTAG AGGTTGTAGA CGTAAACGAC 120
AACGCCCCAG T 131

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Leu Arg Met Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln
1 5 10 15
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu
20 25 30
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGGCTTTGG ATTACGAGGA TCAGAGAGAG TTCCAACATA CAGCTCATAT AAACGACGGA 60
GGTACCCCAG TCTTAGCCAC CAACATCAGC GTGAACGTAT TTGTTACTGA CCGCAATGAT 120
AACGCCCCCT A 131

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Ala Leu Asp Tyr Glu Asp Gln Arg Glu Phe Gln Leu Thr Ala His
 1 5 10 15
 Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
 20 25 30
 Val Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGCGCTTGG ACTACGAGGA GAGTAACAAT TATGAAATTC ACGTGGATGC TACAGATAAA 60
 GGATACCCAC CTATGGTTGC TCACTGCACC GTACTCGTGG GAATCTTGGA TGAAAATGAC 120
 AACGCACCCA T 131

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Lys Arg Leu Asp Tyr Glu Glu Ser Asn Asn Tyr Glu Ile His Val Asp
 1 5 10 15
 Ala Thr Asp Lys Gly Tyr Pro Pro Met Val Ala His Cys Thr Val Leu
 20 25 30
 Val Gly Ile Leu Asp Glu Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAACCGGTGG ACTACGAGAA AGTCAAAGAC TATACCATCG AGATCGTGGC TGTGGATTCC	60
GGCAACCCTC CACTCTCTAG CACCAACTCC CTCAAGGTGC AGGTGGTAGA CGTCAACGAT	120
AACGCCCCCTC T	131

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Lys	Pro	Val	Asp	Tyr	Glu	Lys	Val	Lys	Asp	Tyr	Thr	Ile	Glu	Ile	Val
1				5				10					15		
Ala	Val	Asp	Ser	Gly	Asn	Pro	Pro	Leu	Ser	Ser	Thr	Asn	Ser	Leu	Lys
		20						25					30		
Val	Gln	Val	Val	Asp	Val	Asn	Asp	Asn	Ala	Pro					
		35					40								

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AAGCCTTTTG ATTTGAGGA CACCAAACTC CATGAGATTT ACATCCAGGC CAAAGACAAG	60
GGCGCCAATC CCGAAGGAGC ACATTGCAAA GTGTTGGTGG AGGTTGTGGA TGTGAACGAC	120

AATGCCCTC A

131

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Pro Phe Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln
1 5 10 15
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu
20 25 30
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AAAGGTGTCG ATTACGAGGT GAGTCCACGG CTGCGACTGG TGCTGCAGGC AGAGAGTCGA 60
GGAGCCTTTG CCTTCACTGT GCTGACCCTG ACCCTGCAAG ATGCCAACGA CAACGCCCCG 120
AG 122

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys Gly Val Asp Tyr Glu Val Ser Pro Arg Leu Arg Leu Val Leu Gln
1 5 10 15

Ala Glu Ser Arg Gly Ala Phe Ala Phe Thr Val Leu Thr Leu Thr Leu
20 25 30

Gln Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAAGGGATTG ATTACGAGCA GTTGAGAGAC CTACAGCTGT GGGTGACAGC CAGCGACAGC 60
GGGGACCCGC CTCTTAGCAG CAACGTGTCA CTGAGCCTGT TTGTGCTGGA CCAGAACGAC 120
AACGCCCCCC T 131

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Lys Gly Ile Asp Tyr Glu Gln Leu Arg Asp Leu Gln Leu Trp Val Thr
1 5 10 15

Ala Ser Asp Ser Gly Asp Pro Pro Leu Ser Ser Asn Val Ser Leu Ser
20 25 30

Leu Phe Val Leu Asp Gln Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAGGCGGTTCG ATTTTGAGCG CACATCCTCT TATCAACTCA TCATTCAGGC CACCAATATG 60
GCAGGAATGG CTTCCAATGC TACAGTCAAT ATTCAGATTG TTGATGAAAA CGACAACGCC 120
CCCCA 125

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Lys Ala Val Asp Phe Glu Arg Thr Ser Ser Tyr Gln Leu Ile Ile Gln
1 5 10 15
Ala Thr Asn Met Ala Gly Met Ala Ser Asn Ala Thr Val Asn Ile Gln
20 25 30
Ile Val Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAACGGCTAG ACTTTGAAAA GATACAAAAA TATGTTGTAT GGATAGAGGC CAGAGATGGT 60
GGTTTCCCTC CTTTCTCCTC TTACGAGAAA CTTGATATAA CAGTATTAGA TGTCAACGAT 120
AACGCGCCTA A 131

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys Arg Leu Asp Phe Glu Lys Ile Gln Lys Tyr Val Val Trp Ile Glu
1 5 10 15
Ala Arg Asp Gly Gly Phe Pro Pro Phe Ser Ser Tyr Glu Lys Leu Asp
20 25 30
Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGGGGATCG ATTATGAGAA GGTCAAAGAC TACACCATTG AGATTGTGGC TGTGGACTCT 60
GGCAACCCCC CACTCTCCAG CACTAACTCC CTCAAGGTGC AGGTGGTGGA CGTCAATGAC 120
AACGCACCGT G 131

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Lys Gly Ile Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val
1 5 10 15
Ala Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys
20 25 30
Val Gln Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
AAGGGACTCG ACTACGAGGA TCGGCGGGAA TTTGAATTAA CAGTCATAT CAGCGATGGG      60
GGCACCCCGG TCCTAGCCAC CAACATCAGC GTGAACATAT TTGTCACTGA TCGCAACGAT      120
AATGCCCCCG T                                     131
```

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
Lys Gly Leu Asp Tyr Glu Asp Arg Arg Glu Phe Glu Leu Thr Ala His
1           5           10           15
Ile Ser Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
20           25           30
Ile Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
35           40
```

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
AAGGGTTTGG ACTACGAGAC CACACAGGCC TACCAGCTCA CGGTCAACGC CACAGATCAA      60
GACAACACCA GGCCTCTGTC CACCCTGGCC AACTTGGCCA TCATCATCAC AGATGTCCAG      120
```

```

GACATGGACC CCATCTTCAT CAACCTGCCT TACAGCACCA ACATCTACGA GCATTCTCCT      180
CCGGGCACGA CGGTGCGCAT CATCACCGCC ATAGACCAGG ATCAAGGACG TCCCCGGGGC      240
ATTGGCTACA CCATCGTTTC AGGGAATACC AACAGCATCT TTGCCCTGGA CTACATCAGC      300
GGAGTGCTGA CCTTGAATGG CCTGCTGGAC CGGGAGAACC CCCTGTACAG CCATGGCTTC      360
ATCCTGACTG TGAAGGGCAC GGAGCTGAAC GATGACCGCA CCCCATCTGA CGCTACAGTC      420
ACCACGACCT TCAATATCCT GGTATTGAC ATCAACGACA ACGCCCCACT      470

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Lys Gly Leu Asp Tyr Glu Thr Thr Gln Ala Tyr Gln Leu Thr Val Asn
1          5          10          15
Ala Thr Asp Gln Asp Asn Thr Arg Pro Leu Ser Thr Leu Ala Asn Leu
20          25          30
Ala Ile Ile Ile Thr Asp Val Gln Asp Met Asp Pro Ile Phe Ile Asn
35          40          45
Leu Pro Tyr Ser Thr Asn Ile Tyr Glu His Ser Pro Pro Gly Thr Thr
50          55          60
Val Arg Ile Ile Thr Ala Ile Asp Gln Asp Gln Gly Arg Pro Arg Gly
65          70          75          80
Ile Gly Tyr Thr Ile Val Ser Gly Asn Thr Asn Ser Ile Phe Ala Leu
85          90          95
Asp Tyr Ile Ser Gly Val Leu Thr Leu Asn Gly Leu Leu Asp Arg Glu
100         105         110
Asn Pro Leu Tyr Ser Gly Gly Phe Ile Leu Thr Val Lys Gly Thr Glu
115         120         125
Leu Asn Asp Asp Arg Thr Pro Ser Asp Ala Thr Val Thr Thr Thr Phe
130         135         140
Asn Ile Leu Val Ile Asp Ile Asn Asp Asn Ala Pro
145         150         155

```

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
AAGGGGGTCG ATTACGAGGT ACTACAGGCC TTTGAGTTCC ACGTGAGCGC CACAGACCGA      60
GGCTCACCGG GGCTCAGCAG CCAGGCTCTG GTGCGCGTGG TGGTGCTGGA CGACAATGAC      120
AACGCTCCCCG T                                     131
```

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
Lys Gly Val Asp Tyr Glu Val Leu Gln Ala Phe Glu Phe His Val Ser
 1             5             10             15
Ala Thr Asp Arg Gly Ser Pro Gly Leu Ser Ser Gln Ala Leu Val Arg
      20             25             30
Val Val Val Leu Asp Asp Asn Asp Asn Ala Pro
      35             40
```

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
AAGGGGCTGG ATTATGAGCA GTTCCAGACC CTACAACCTGG GAGTGACCGC TAGTGACAGT      60
GGAAACCCAC CATTAAAGAAG CAATATTTCA CTGACCCTTT TCGTGCTGGA CCAGAATGAT      120
```

AACGCCCCAA A

131

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Lys Gly Leu Asp Tyr Glu Gln Phe Gln Thr Leu Gln Leu Gly Val Thr
1 5 10 15
Ala Ser Asp Ser Gly Asn Pro Pro Leu Arg Ser Asn Ile Ser Leu Thr
20 25 30
Leu Phe Val Leu Asp Gln Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AAGCGGGTTG ATTACGAGGA TGTCCAGAAA TACTCGCTGA GCATTAAGGC CCAGGATGGG 60
CGGCCCCCGC TCATCAATTC TTCAGGGGTG GTGTCTGTGC AGGTGCTGGA TGTCAACGAC 120
AATGCCCCGG A 131

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Lys Arg Val Asp Tyr Glu Asp Val Gln Lys Tyr Ser Leu Ser Ile Lys
1 5 10 15

Ala Gln Asp Gly Arg Pro Pro Leu Ile Asn Ser Ser Gly Val Val Ser
20 25 30

Val Gln Val Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AAACCGGTAG ACTTTGAGCT ACAGCAGTTC TATGAAGTAG CTGTGGTGGC TTGGAAGTCT	60
GAGGGATTTC ATGTCAAAAG GGTCAATAAA GTGCAACTTT TAGATGACAA CGACAATGCC	120
CCGAT	125

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Pro Val Asp Phe Glu Leu Gln Gln Phe Tyr Glu Val Ala Val Val	
1 5 10 15	
Ala Trp Asn Ser Glu Gly Phe His Val Lys Arg Val Ile Lys Val Gln	
20 25 30	
Leu Leu Asp Asp Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGGGATTAG ATTTTGAAAC TTTGCCCAT TACACATTGA TAATACAAGG AACTAACATG	60
GCTGGTTTGT CCACTAATAC AACGGTTCTA GTTCACTTGC AGGATGAGAA TGATAACGCC	120
CCAAA	125

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Lys	Gly	Leu	Asp	Phe	Glu	Thr	Leu	Pro	Ile	Tyr	Thr	Leu	Ile	Ile	Gln
1				5					10					15	
Gly	Thr	Asn	Met	Ala	Gly	Leu	Ser	Thr	Asn	Thr	Thr	Val	Leu	Val	His
		20					25						30		
Leu	Gln	Asp	Glu	Asn	Asp	Asn	Ala	Pro							
		35					40								

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AAGCGGGCGG ATTTTCGAGGC GATCCGGGAG TACAGTCTGA GGATCAAAGC GCAGGACGGG	60
GGGCGGCCTC CCCTCAGCAA CACCACGGGC ATGGTCACAG TGCAGGTCGT GGACGTCAAT	120
GACAACGCAC CCCT	134

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Lys Arg Ala Asp Phe Glu Ala Ile Arg Glu Tyr Ser Leu Arg Ile Lys
 1 5 10 15
 Ala Gln Asp Gly Gly Arg Pro Pro Leu Ser Asn Thr Thr Gly Met Val
 20 25 30
 Thr Val Gln Val Val Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAGCGGTTGG ATTACGAAAA GGCATCGGAA TATGAAATCT ATGTTCAAGC CGCTGACAAA 60
 GCGCTGTCC CTATGGCTGG CCATTGCAAA GTGTGCTGG AGATCGTGGA TGTCAACGAC 120
 AACGCCCCCT T 131

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Lys Arg Leu Asp Tyr Glu Lys Ala Ser Glu Tyr Glu Ile Tyr Val Gln
 1 5 10 15
 Ala Ala Asp Lys Gly Ala Val Pro Met Ala Gly His Cys Lys Val Leu
 20 25 30
 Leu Glu Ile Val Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AAGGGGATCG ATTATGAGGA TCAGGTCTCT TACACATTAG CAGTAACAGC ACATGACTAT 60
GGCATCCCTC AAAAATCAGA CACTACCTAT TTGGAAATCT TAGTAATTGA TGTTAACGAC 120
AACGCGCCCC A 131

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Lys Gly Ile Asp Tyr Glu Asp Gln Val Ser Tyr Thr Leu Ala Val Thr
1 5 10 15
Ala His Asp Tyr Gly Ile Pro Gln Lys Ser Asp Thr Thr Tyr Leu Glu
20 25 30
Ile Leu Val Ile Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AAAGGGTTAG ATTTTCGAGGG CACTAAAGAT TCAGCGTTTA AAATAGTGGC AGCTGACACA 60
GGGAAGCCCA GCCTCAACCA GACAGCCCTG GTGAGAGTAG AGCTGGAGGA TGAGAACGAC 120

AACGCCCCAA T

131

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys	Gly	Leu	Asp	Phe	Glu	Gly	Thr	Lys	Asp	Ser	Ala	Phe	Lys	Ile	Val
1				5				10					15		
Ala	Ala	Asp	Thr	Gly	Lys	Pro	Ser	Leu	Asn	Gln	Thr	Ala	Leu	Val	Arg
			20					25					30		
Val	Glu	Leu	Glu	Asp	Glu	Asn	Asp	Asn	Ala	Pro					
		35				40									

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGGTGTGG	ATTTTGAAAG	TGTGCGTAGC	TACAGGCTGG	TTATTCGTGC	TCAAGATGGA	60
GGCAGCCCCT	CCAGAAGTAA	CACCACCCAG	CTCTTGGTCA	ACGTCATCGA	TCGAATGACA	120
ATGCGCCGCT						130

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Lys	Gly	Val	Asp	Phe	Glu	Ser	Val	Arg	Ser	Tyr	Arg	Leu	Val	Ile	Arg
1				5				10					15		

Ala Gln Asp Gly Gly Ser Pro Ser Arg Ser Asn Thr Thr Gln Leu Leu
20 25 30

Val Asn Val Ile Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AAGGGTGTGG ACTTCGAGCT GACACATCTG TATGAGATTT GGATTGAGGC TGCCGATGGA 60
GACACGCCAA GTCTGCGTAG TGTAAC TCTT ATAACGCTCA ACGTAACGGA TGCCAATGAC 120
AATGCTCCCA A 131

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Lys Gly Val Asp Phe Glu Leu Thr His Leu Tyr Glu Ile Trp Ile Glu
1 5 10 15
Ala Ala Asp Gly Asp Thr Pro Ser Leu Arg Ser Val Thr Leu Ile Thr
20 25 30
Leu Asn Val Thr Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAAGGCGTTT GATTTTGAAG AGACAAGTAG ATATGTGTTG AGTGTGGAAG CTAAGGATGG	60
AGGAGTACAC ACAGCTCACT GTAATGTTCA AATAGAAATT GTTGACGAGA ATGACAATGC	120
CCCAGAGGTG ACATTCATGT CCTTCTCTAA CCAGATTCCA GAGGATTCAG ACCTTGGAAC	180
TGTAATAGCC CTCATAAAAG TCGAGACAA GGATTCTGGG CAAAATGGCA TGGTGACATG	240
CTATACTCAG GAAGAAGTTC CTTTCAAATT AGAATCCACC TCGAAGAATT ATTACAAGCT	300
GGTGATTGCT GGAGCCCTAA ACCGGGAGCA GACAGCAGAC TACAACGTCA CAATCATAGC	360
CACCGACAAG GGCAAACCAG CCCTTTCCTC CAGGACAAGC ATCACCTGC ACATCTCCGA	420
CATCAACGAT AATGCCCCCG T	441

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Lys	Ala	Phe	Asp	Phe	Glu	Glu	Thr	Ser	Arg	Tyr	Val	Leu	Ser	Val	Glu	1	5	10	15
Ala	Lys	Asp	Gly	Gly	Val	His	Thr	Ala	His	Cys	Asn	Val	Gln	Ile	Glu	20	25	30	
Ile	Val	Asp	Glu	Asn	Asp	Asn	Ala	Pro	Glu	Val	Thr	Phe	Met	Ser	Phe	35	40	45	
Ser	Asn	Gln	Ile	Pro	Glu	Asp	Ser	Asp	Leu	Gly	Thr	Val	Ile	Ala	Leu	50	55	60	
Ile	Lys	Val	Arg	Asp	Lys	Asp	Ser	Gly	Gln	Asn	Gly	Met	Val	Thr	Cys	65	70	75	80
Tyr	Thr	Gln	Glu	Glu	Val	Pro	Phe	Lys	Leu	Glu	Ser	Thr	Ser	Lys	Asn	85	90	95	
Tyr	Tyr	Lys	Leu	Val	Ile	Ala	Gly	Ala	Leu	Asn	Arg	Glu	Gln	Thr	Ala	100	105	110	
Asp	Tyr	Asn	Val	Thr	Ile	Ile	Ala	Thr	Asp	Lys	Gly	Lys	Pro	Ala	Leu	115	120	125	
Ser	Ser	Arg	Thr	Ser	Ile	Thr	Leu	His	Ile	Ser	Asp	Ile	Asn	Asp	Asn	130	135	140	
Ala	Pro															145			

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
AAGCGAGTGG ATTACGAGGC CACTCGGAAT TATAAGCTGA GAGTTAAGGC TACTGATCTT      60
GGGATTCCAC CGAGATCTTC TAACATGACA CTGTTTCATTC ATGTCCTTGA TGTTAACGAC      120
AACGCTCCCT T                                131
```

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
Lys Arg Val Asp Tyr Glu Ala Thr Arg Asn Tyr Lys Leu Arg Val Lys
1           5           10
Ala Thr Asp Leu Gly Ile Pro Pro Arg Ser Ser Asn Met Thr Leu Phe
20          25          30
Ile His Val Leu Asp Val Asn Asp Asn Ala Pro
35          40
```

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 495..3572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTCTATTTCG ACATTCTCTT TGGATTGTTT TGCTATAACT TGAAATTTGG GATGTCACAA	60
ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTTCTGCT AATCTCCCAG GCTGGCAGCA	120
TTGGAGACTT GCTGACTTCT TTCATCCCCC ACTCTTTTCA CCTGAAATTC CTTTCCTTGG	180
TTTGTCTCTA AGTCCTATGC TTCAGTCAGG GGCCAACCAA ATCTCACTGC CTCCTTTTTA	240
TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT	300
ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCACT	360
CGTTTTTCGTA CCTCTTCATG GTGATGGGGA GCCCTTTTGA GGTGGTGACT GTGCTTTATA	420
CTCCTCATGA TGCTTCACAT GTGGCAGGCG TGGAGTGCCC GGAGGCGGCC CTCCTGATTC	480
TGGGGCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG	530
Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly	
1 5 10	
CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG	578
Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu	
15 20 25	
GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG	626
Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu	
30 35 40	
GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT	674
Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly	
45 50 55 60	
TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC	722
Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr	
65 70 75	
CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC	770
Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser	
80 85 90	
ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT	818
Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp	
95 100 105	
CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT	866
Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn	
110 115 120	
GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT	914
Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn	
125 130 135 140	
GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT	962
Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro	
145 150 155	
GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC	1010
Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp	
160 165 170	

CGT	GAT	GCT	GGT	CCC	AAC	GGT	GTG	GCA	TCC	TAT	GAG	CTG	CAG	GTG	GCA	1058
Arg	Asp	Ala	Gly	Pro	Asn	Gly	Val	Ala	Ser	Tyr	Glu	Leu	Gln	Val	Ala	
		175					180					185				
GAG	GAC	CAG	GAG	GAG	AAG	CAA	CCA	CAG	CTC	ATT	GTG	ATG	GGC	AAC	CTG	1106
Glu	Asp	Gln	Glu	Glu	Lys	Gln	Pro	Gln	Leu	Ile	Val	Met	Gly	Asn	Leu	
		190				195					200					
GAC	CGT	GAG	CGC	TGG	GAC	TCC	TAT	GAC	CTC	ACC	ATC	AAG	GTG	CAG	GAT	1154
Asp	Arg	Glu	Arg	Trp	Asp	Ser	Tyr	Asp	Leu	Thr	Ile	Lys	Val	Gln	Asp	
205					210					215					220	
GGC	GGC	AGC	CCC	CCA	CGC	GCC	ACG	AGT	GCC	CTG	CTG	CGT	GTC	ACC	GTG	1202
Gly	Gly	Ser	Pro	Pro	Arg	Ala	Thr	Ser	Ala	Leu	Leu	Arg	Val	Thr	Val	
				225					230					235		
CTT	GAC	ACC	AAT	GAC	AAC	GCC	CCC	AAG	TTT	GAG	CGG	CCC	TCC	TAT	GAG	1250
Leu	Asp	Thr	Asn	Asp	Asn	Ala	Pro	Lys	Phe	Glu	Arg	Pro	Ser	Tyr	Glu	
			240					245					250			
GCC	GAA	CTA	TCT	GAG	AAT	AGC	CCC	ATA	GGC	CAC	TCG	GTC	ATC	CAG	GTG	1298
Ala	Glu	Leu	Ser	Glu	Asn	Ser	Pro	Ile	Gly	His	Ser	Val	Ile	Gln	Val	
		255					260					265				
AAG	GCC	AAT	GAC	TCA	GAC	CAA	GGT	GCC	AAT	GCA	GAA	ATC	GAA	TAC	ACA	1346
Lys	Ala	Asn	Asp	Ser	Asp	Gln	Gly	Ala	Asn	Ala	Glu	Ile	Glu	Tyr	Thr	
		270				275					280					
TTC	CAC	CAG	GCG	CCC	GAA	GTT	GTG	AGG	CGT	CTT	CTT	CGA	CTG	GAC	AGG	1394
Phe	His	Gln	Ala	Pro	Glu	Val	Val	Arg	Arg	Leu	Leu	Arg	Leu	Asp	Arg	
285					290					295					300	
AAC	ACT	GGA	CTT	ATC	ACT	GTT	CAG	GGC	CCG	GTG	GAC	CGT	GAG	GAC	CTA	1442
Asn	Thr	Gly	Leu	Ile	Thr	Val	Gln	Gly	Pro	Val	Asp	Arg	Glu	Asp	Leu	
				305					310					315		
AGC	ACC	CTG	CGC	TTC	TCA	GTG	CTT	GCT	AAG	GAC	CGA	GGC	ACC	AAC	CCC	1490
Ser	Thr	Leu	Arg	Phe	Ser	Val	Leu	Ala	Lys	Asp	Arg	Gly	Thr	Asn	Pro	
			320					325					330			
AAG	AGT	GCC	CGT	GCC	CAG	GTG	GTT	GTG	ACC	GTG	AAG	GAC	ATG	AAT	GAC	1538
Lys	Ser	Ala	Arg	Ala	Gln	Val	Val	Val	Thr	Val	Lys	Asp	Met	Asn	Asp	
		335				340						345				
AAT	GCC	CCC	ACC	ATT	GAG	ATC	CGG	GGC	ATA	GGG	CTA	GTG	ACT	CAT	CAA	1586
Asn	Ala	Pro	Thr	Ile	Glu	Ile	Arg	Gly	Ile	Gly	Leu	Val	Thr	His	Gln	
		350				355					360					
GAT	GGG	ATG	GCT	AAC	ATC	TCA	GAG	GAT	GTG	GCA	GAG	GAG	ACA	GCT	GTG	1634
Asp	Gly	Met	Ala	Asn	Ile	Ser	Glu	Asp	Val	Ala	Glu	Glu	Thr	Ala	Val	
365					370					375					380	
GCC	CTG	GTG	CAG	GTG	TCT	GAC	CGA	GAT	GAG	GGA	GAG	AAT	GCA	GCT	GTC	1682
Ala	Leu	Val	Gln	Val	Ser	Asp	Arg	Asp	Glu	Gly	Glu	Asn	Ala	Ala	Val	
				385					390					395		
ACC	TGT	GTG	GTG	GCA	GGT	GAT	GTG	CCC	TTC	CAG	CTG	CGC	CAG	GCC	AGT	1730
Thr	Cys	Val	Val	Ala	Gly	Asp	Val	Pro	Phe	Gln	Leu	Arg	Gln	Ala	Ser	
			400					405					410			

GAG Glu	ACA Thr	GGC Gly 415	AGT Ser	GAC Asp	AGC Ser	AAG Lys	AAG Lys 420	AAG Lys	TAT Tyr	TTC Phe	CTG Leu	CAG Gln 425	ACT Thr	ACC Thr	ACC Thr	1778
CCG Pro	CTA Leu 430	GAC Asp	TAC Tyr	GAG Glu	AAG Lys	GTC Val 435	AAA Lys	GAC Asp	TAC Tyr	ACC Thr	ATT Ile 440	GAG Glu	ATT Ile	GTG Val	GCT Ala	1826
GTG Val 445	GAC Asp	TCT Ser	GGC Gly	AAC Asn	CCC Pro 450	CCA Pro	CTC Leu	TCC Ser	AGC Ser	ACT Thr 455	AAC Asn	TCC Ser	CTC Leu	AAG Lys	GTG Val 460	1874
CAG Gln	GTG Val	GTG Val	GAC Asp	GTC Val 465	AAT Asn	GAC Asp	AAC Asn	GCA Ala	CCT Pro 470	GTC Val	TTC Phe	ACT Thr	CAG Gln	AGT Ser 475	GTC Val	1922
ACT Thr	GAG Glu	GTC Val 480	GCC Ala	TTC Phe	CCG Pro	GAA Glu	AAC Asn 485	AAC Asn	AAG Lys	CCT Pro	GGT Gly	GAA Glu 490	GTG Val	ATT Ile	GCT Ala	1970
GAG Glu	ATC Ile	ACT Thr 495	GCC Ala	AGT Ser	GAT Asp	GCT Ala	GAC Asp 500	TCT Ser	GGC Gly	TCT Ser	AAT Asn 505	GCT Ala	GAG Glu	CTG Leu	GTT Val	2018
TAC Tyr	TCT Ser 510	CTG Leu	GAG Glu	CCT Pro	GAG Glu	CCG Pro 515	GCT Ala	GCT Ala	AAG Lys	GGC Gly	CTC Leu 520	TTC Phe	ACC Thr	ATC Ile	TCA Ser	2066
CCC Pro 525	GAG Glu	ACT Thr	GGA Gly	GAG Glu	ATC Ile 530	CAG Gln	GTG Val	AAG Lys	ACA Thr	TCT Ser 535	CTG Leu	GAT Asp	CGG Arg	GAA Glu	CAG Gln 540	2114
CGG Arg	GAG Glu	AGC Ser	TAT Tyr	GAG Glu 545	TTG Leu	AAG Lys	GTG Val	GTG Val	GCA Ala 550	GCT Ala	GAC Asp	CGG Arg	GGC Gly	AGT Ser 555	CCT Pro	2162
AGC Ser	CTC Leu	CAG Gln	GGC Gly 560	ACA Thr	GCC Ala	ACT Thr	GTC Val 565	CTT Leu	GTC Val	AAT Asn	GTG Val	CTG Leu	GAC Asp 570	TGC Cys	AAT Asn	2210
GAC Asp	AAT Asn	GAC Asp 575	CCC Pro	AAA Lys	TTT Phe	ATG Met	CTG Leu 580	AGT Ser	GGC Gly	TAC Tyr	AAC Asn	TTC Phe 585	TCA Ser	GTG Val	ATG Met	2258
GAG Glu	AAC Asn 590	ATG Met	CCA Pro	GCA Ala	CTG Leu	AGT Ser 595	CCA Pro	GTG Val	GGC Gly	ATG Met	GTG Val 600	ACT Thr	GTC Val	ATT Ile	GAT Asp	2306
GGA Gly 605	GAC Asp	AAG Lys	GGG Gly	GAG Glu	AAT Asn 610	GCC Ala	CAG Gln	GTG Val	CAG Gln	CTC Leu 615	TCA Ser	GTG Val	GAG Glu	CAG Gln	GAC Asp 620	2354
AAC Asn	GGT Gly	GAC Asp	TTT Phe	GTT Val 625	ATC Ile	CAG Gln	AAT Asn	GGC Gly	ACA Thr 630	GGC Gly	ACC Thr	ATC Ile	CTA Leu	TCC Ser 635	AGC Ser	2402
CTG Leu	AGC Ser	TTT Phe 640	GAT Asp	CGA Arg	GAG Glu	CAA Gln	CAA Gln	AGC Ser 645	ACC Thr	TAC Tyr	ACC Thr	TTC Phe	CAG Gln 650	CTG Leu	AAG Lys	2450

GCA	GTG	GAT	GGT	GGC	GTC	CCA	CCT	CGC	TCA	GCT	TAC	GTT	GGT	GTC	ACC	2498
Ala	Val	Asp	Gly	Gly	Val	Pro	Pro	Arg	Ser	Ala	Tyr	Val	Gly	Val	Thr	
	655						660					665				
ATC	AAT	GTG	CTG	GAC	GAG	AAT	GAC	AAC	GCA	CCC	TAT	ATC	ACT	GCC	CCT	2546
Ile	Asn	Val	Leu	Asp	Glu	Asn	Asp	Asn	Ala	Pro	Tyr	Ile	Thr	Ala	Pro	
	670					675					680					
TCT	AAC	ACC	TCT	CAC	AAG	CTG	CTG	ACC	CCC	CAG	ACA	CGT	CTT	GGT	GAG	2594
Ser	Asn	Thr	Ser	His	Lys	Leu	Leu	Thr	Pro	Gln	Thr	Arg	Leu	Gly	Glu	
685					690					695					700	
ACG	GTC	AGC	CAG	GTG	GCA	GCC	GAG	GAC	TTT	GAC	TCT	GGT	GTC	AAT	GCC	2642
Thr	Val	Ser	Gln	Val	Ala	Ala	Glu	Asp	Phe	Asp	Ser	Gly	Val	Asn	Ala	
				705					710					715		
GAG	CTG	ATC	TAC	AGC	ATT	GCA	GGT	GGC	AAC	CCT	TAT	GGA	CTC	TTC	CAG	2690
Glu	Leu	Ile	Tyr	Ser	Ile	Ala	Gly	Gly	Asn	Pro	Tyr	Gly	Leu	Phe	Gln	
			720					725					730			
ATT	GGG	TCA	CAT	TCA	GGT	GCC	ATC	ACC	CTG	GAG	AAG	GAG	ATT	GAG	CGG	2738
Ile	Gly	Ser	His	Ser	Gly	Ala	Ile	Thr	Leu	Glu	Lys	Glu	Ile	Glu	Arg	
	735					740					745					
CGC	CAC	CAT	GGG	CTA	CAC	CGC	CTG	GTG	GTG	AAG	GTC	AGT	GAC	CGC	GGC	2786
Arg	His	His	Gly	Leu	His	Arg	Leu	Val	Val	Lys	Val	Ser	Asp	Arg	Gly	
	750					755					760					
AAG	CCC	CCA	CGC	TAT	GGC	ACA	GCC	TTG	GTC	CAT	CTT	TAT	GTC	AAT	GAG	2834
Lys	Pro	Pro	Arg	Tyr	Gly	Thr	Ala	Leu	Val	His	Leu	Tyr	Val	Asn	Glu	
765					770					775					780	
ACT	CTG	GCC	AAC	CGC	ACG	CTG	CTG	GAG	ACC	CTC	CTG	GGC	CAC	AGC	CTG	2882
Thr	Leu	Ala	Asn	Arg	Thr	Leu	Leu	Glu	Thr	Leu	Leu	Gly	His	Ser	Leu	
				785					790					795		
GAC	ACG	CCG	CTG	GAT	ATT	GAC	ATT	GCT	GGG	GAT	CCA	GAA	TAT	GAG	CGC	2930
Asp	Thr	Pro	Leu	Asp	Ile	Asp	Ile	Ala	Gly	Asp	Pro	Glu	Tyr	Glu	Arg	
		800						805					810			
TCC	AAG	CAG	CGT	GGC	AAC	ATT	CTC	TTT	GGT	GTG	GTG	GCT	GGT	GTG	GTG	2978
Ser	Lys	Gln	Arg	Gly	Asn	Ile	Leu	Phe	Gly	Val	Val	Ala	Gly	Val	Val	
	815						820					825				
GCC	GTG	GCC	TTG	CTC	ATC	GCC	CTG	GCG	GTT	CTT	GTG	CGC	TAC	TGC	AGA	3026
Ala	Val	Ala	Leu	Leu	Ile	Ala	Leu	Ala	Val	Leu	Val	Arg	Tyr	Cys	Arg	
	830					835					840					
CAG	CGG	GAG	GCC	AAA	AGT	GGT	TAC	CAG	GCT	GGT	AAG	AAG	GAG	ACC	AAG	3074
Gln	Arg	Glu	Ala	Lys	Ser	Gly	Tyr	Gln	Ala	Gly	Lys	Lys	Glu	Thr	Lys	
845					850					855					860	
GAC	CTG	TAT	GCC	CCC	AAG	CCC	AGT	GGC	AAG	GCC	TCC	AAG	GGA	AAC	AAA	3122
Asp	Leu	Tyr	Ala	Pro	Lys	Pro	Ser	Gly	Lys	Ala	Ser	Lys	Gly	Asn	Lys	
				865					870					875		
AGC	AAA	GGC	AAG	AAG	AGC	AAG	TCC	CCA	AAG	CCC	GTG	AAG	CCA	GTG	GAG	3170
Ser	Lys	Gly	Lys	Lys	Ser	Lys	Ser	Pro	Lys	Pro	Val	Lys	Pro	Val	Glu	
			880					885					890			

GAC GAG GAT GAG GCC GGG CTG CAG AAG TCC CTC AAG TTC AAC CTG ATG Asp Glu Asp Glu Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met 895 900 905	3218
AGC GAT GCC CCT GGG GAC AGT CCC CGC ATC CAC CTG CCC CTC AAC TAC Ser Asp Ala Pro Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr 910 915 920	3266
CCA CCA GGC AGC CCT GAC CTG GGC CGC CAC TAT CGC TCT AAC TCC CCA Pro Pro Gly Ser Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro 925 930 935 940	3314
CTG CCT TCC ATC CAG CTG CAG CCC CAG TCA CCC TCA GCC TCC AAG AAG Leu Pro Ser Ile Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys 945 950 955	3362
CAC CAG GTG GTA CAG GAC CTG CCA CCT GCA AAC ACA TTC GTG GGC ACC His Gln Val Val Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr 960 965 970	3410
GGG GAC ACC ACG TCC ACG GGC TCT GAG CAG TAC TCC GAC TAC AGC TAC Gly Asp Thr Thr Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr 975 980 985	3458
CGC ACC AAC CCC CCC AAA TAC CCC AGC AAG CAG GTA GGC CAG CCC TTT Arg Thr Asn Pro Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe 990 995 1000	3506
CAG CTC AGC ACA CCC CAG CCC CTA CCC CAC CCC TAC CAC GGA GCC ATC Gln Leu Ser Thr Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile 1005 1010 1015 1020	3554
TGG ACC GAG GTG TGG GAG TGATGGAGCA GGTTTACTGT GCCTGCCCCGT Trp Thr Glu Val Trp Glu 1025	3602
GTGTTGGGGGCC AGCCTGAGCC AGCAGTGGGA GGTGGGGCCT TAGTGCCTCA CCGGGCACAC	3662
GGATTAGGCT GAGTGAAGAT TAAGGGAGGG TGTGCTCTGT GGTCTCCTCC CTGCCCTCTC	3722
CCCCTGGGG AGAGACCTGT GATTTGCCAA GTCCCTGGAC CCTGGACCAG CTTACTGGGCC	3782
TTATGGGTTG GGGGTGGTAG GCAGGTGAGC GTAAGTGGGG AGGGAAATGG GTAAGAAGTC	3842
TACTCCAAAC CTAGGTCTCT ATGTCAGACC AGACCTAGGT GCTTCTCTAG GAGGGAAACA	3902
GGGAGACCTG GGGTCCTGTG GATAACTGAG TGGGGAGTCT GCCAGGGGAG GGCACCTTCC	3962
CATTGTGCCT TCTGTGTGTA TTGTGCATTA ACCTCTTCCT CACCACTAGG CTTCTGGGGC	4022
TGGGTCCCAC ATGCCCTTGA CCCTGACAAT AAAGTTCTCT ATTTTGGAA AAAAAAAAAA	4082
AAAAAAAAAA AAAAAAAAAA AA	4104

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly Gln Arg Leu Leu
1 5 10 15
Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Ala Pro Ser Pro
20 25 30
Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu Glu Gln Pro Pro
35 40 45
Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly Phe Pro Asp Val
50 55 60
Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
65 70 75 80
Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser Ile Asp Arg Glu
85 90 95
Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
100 105 110
Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
115 120 125
Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
130 135 140
Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
145 150 155 160
Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
165 170 175
Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
180 185 190
Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
195 200 205
Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly Ser Pro
210 215 220
Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
225 230 235 240
Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
245 250 255
Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
260 265 270

Ser	Asp	Gln	Gly	Ala	Asn	Ala	Glu	Ile	Glu	Tyr	Thr	Phe	His	Gln	Ala		
		275					280					285					
Pro	Glu	Val	Val	Arg	Arg	Leu	Leu	Arg	Leu	Asp	Arg	Asn	Thr	Gly	Leu		
		290				295					300						
Ile	Thr	Val	Gln	Gly	Pro	Val	Asp	Arg	Glu	Asp	Leu	Ser	Thr	Leu	Arg		
305					310					315					320		
Phe	Ser	Val	Leu	Ala	Lys	Asp	Arg	Gly	Thr	Asn	Pro	Lys	Ser	Ala	Arg		
				325					330					335			
Ala	Gln	Val	Val	Val	Thr	Val	Lys	Asp	Met	Asn	Asp	Asn	Ala	Pro	Thr		
			340					345					350				
Ile	Glu	Ile	Arg	Gly	Ile	Gly	Leu	Val	Thr	His	Gln	Asp	Gly	Met	Ala		
		355					360					365					
Asn	Ile	Ser	Glu	Asp	Val	Ala	Glu	Glu	Thr	Ala	Val	Ala	Leu	Val	Gln		
		370				375					380						
Val	Ser	Asp	Arg	Asp	Glu	Gly	Glu	Asn	Ala	Ala	Val	Thr	Cys	Val	Val		
385					390					395					400		
Ala	Gly	Asp	Val	Pro	Phe	Gln	Leu	Arg	Gln	Ala	Ser	Glu	Thr	Gly	Ser		
				405					410					415			
Asp	Ser	Lys	Lys	Lys	Tyr	Phe	Leu	Gln	Thr	Thr	Thr	Pro	Leu	Asp	Tyr		
			420					425					430				
Glu	Lys	Val	Lys	Asp	Tyr	Thr	Ile	Glu	Ile	Val	Ala	Val	Asp	Ser	Gly		
		435				440					445						
Asn	Pro	Pro	Leu	Ser	Ser	Thr	Asn	Ser	Leu	Lys	Val	Gln	Val	Val	Asp		
		450				455					460						
Val	Asn	Asp	Asn	Ala	Pro	Val	Phe	Thr	Gln	Ser	Val	Thr	Glu	Val	Ala		
465					470					475					480		
Phe	Pro	Glu	Asn	Asn	Lys	Pro	Gly	Glu	Val	Ile	Ala	Glu	Ile	Thr	Ala		
				485				490						495			
Ser	Asp	Ala	Asp	Ser	Gly	Ser	Asn	Ala	Glu	Leu	Val	Tyr	Ser	Leu	Glu		
			500					505					510				
Pro	Glu	Pro	Ala	Ala	Lys	Gly	Leu	Phe	Thr	Ile	Ser	Pro	Glu	Thr	Gly		
		515					520					525					
Glu	Ile	Gln	Val	Lys	Thr	Ser	Leu	Asp	Arg	Glu	Gln	Arg	Glu	Ser	Tyr		
		530				535					540						
Glu	Leu	Lys	Val	Val	Ala	Ala	Asp	Arg	Gly	Ser	Pro	Ser	Leu	Gln	Gly		
545					550					555					560		
Thr	Ala	Thr	Val	Leu	Val	Asn	Val	Leu	Asp	Cys	Asn	Asp	Asn	Asp	Pro		
				565					570					575			
Lys	Phe	Met	Leu	Ser	Gly	Tyr	Asn	Phe	Ser	Val	Met	Glu	Asn	Met	Pro		
			580					585					590				

Ala	Leu	Ser	Pro	Val	Gly	Met	Val	Thr	Val	Ile	Asp	Gly	Asp	Lys	Gly	595	600	605
Glu	Asn	Ala	Gln	Val	Gln	Leu	Ser	Val	Glu	Gln	Asp	Asn	Gly	Asp	Phe	610	615	620
Val	Ile	Gln	Asn	Gly	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Leu	Ser	Phe	Asp	625	630	635
Arg	Glu	Gln	Gln	Ser	Thr	Tyr	Thr	Phe	Gln	Leu	Lys	Ala	Val	Asp	Gly	645	650	655
Gly	Val	Pro	Pro	Arg	Ser	Ala	Tyr	Val	Gly	Val	Thr	Ile	Asn	Val	Leu	660	665	670
Asp	Glu	Asn	Asp	Asn	Ala	Pro	Tyr	Ile	Thr	Ala	Pro	Ser	Asn	Thr	Ser	675	680	685
His	Lys	Leu	Leu	Thr	Pro	Gln	Thr	Arg	Leu	Gly	Glu	Thr	Val	Ser	Gln	690	695	700
Val	Ala	Ala	Glu	Asp	Phe	Asp	Ser	Gly	Val	Asn	Ala	Glu	Leu	Ile	Tyr	705	710	715
Ser	Ile	Ala	Gly	Gly	Asn	Pro	Tyr	Gly	Leu	Phe	Gln	Ile	Gly	Ser	His	725	730	735
Ser	Gly	Ala	Ile	Thr	Leu	Glu	Lys	Glu	Ile	Glu	Arg	Arg	His	His	Gly	740	745	750
Leu	His	Arg	Leu	Val	Val	Lys	Val	Ser	Asp	Arg	Gly	Lys	Pro	Pro	Arg	755	760	765
Tyr	Gly	Thr	Ala	Leu	Val	His	Leu	Tyr	Val	Asn	Glu	Thr	Leu	Ala	Asn	770	775	780
Arg	Thr	Leu	Leu	Glu	Thr	Leu	Leu	Gly	His	Ser	Leu	Asp	Thr	Pro	Leu	785	790	795
Asp	Ile	Asp	Ile	Ala	Gly	Asp	Pro	Glu	Tyr	Glu	Arg	Ser	Lys	Gln	Arg	805	810	815
Gly	Asn	Ile	Leu	Phe	Gly	Val	Val	Ala	Gly	Val	Val	Ala	Val	Ala	Leu	820	825	830
Leu	Ile	Ala	Leu	Ala	Val	Leu	Val	Arg	Tyr	Cys	Arg	Gln	Arg	Glu	Ala	835	840	845
Lys	Ser	Gly	Tyr	Gln	Ala	Gly	Lys	Lys	Glu	Thr	Lys	Asp	Leu	Tyr	Ala	850	855	860
Pro	Lys	Pro	Ser	Gly	Lys	Ala	Ser	Lys	Gly	Asn	Lys	Ser	Lys	Gly	Lys	865	870	875
Lys	Ser	Lys	Ser	Pro	Lys	Pro	Val	Lys	Pro	Val	Glu	Asp	Glu	Asp	Glu	885	890	895
Ala	Gly	Leu	Gln	Lys	Ser	Leu	Lys	Phe	Asn	Leu	Met	Ser	Asp	Ala	Pro	900	905	910

Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr Pro Pro Gly Ser
 915 920 925

Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro Leu Pro Ser Ile
 930 935 940

Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys His Gln Val Val
 945 950 955 960

Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr Gly Asp Thr Thr
 965 970 975

Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr Arg Thr Asn Pro
 980 985 990

Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe Gln Leu Ser Thr
 995 1000 1005

Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile Trp Thr Glu Val
 1010 1015 1020

Trp Glu
 1025

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 115..2827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAAGCGCT AACCCGCTGA AAGTTTCTCA	60
GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTTGAG TGAG ATG	117
	Met
	1
GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG	165
Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val	
	5 10 15
GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT	213
Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile	
	20 25 30
CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC	261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn	
	35 40 45

GTG	GTC	GCG	AAC	CTT	GGT	TTG	GAT	CTC	GGT	AGC	CTC	TCA	GCC	CGC	AGG	309
Val	Val	Ala	Asn	Leu	Gly	Leu	Asp	Leu	Gly	Ser	Leu	Ser	Ala	Arg	Arg	
50					55					60					65	
TTC	CCG	GTG	GTG	TCT	GGA	GCT	AGC	CGA	AGA	TTC	TTT	GAG	GTG	AAC	CGG	357
Phe	Pro	Val	Val	Ser	Gly	Ala	Ser	Arg	Arg	Phe	Phe	Glu	Val	Asn	Arg	
				70					75					80		
GAG	ACC	GGA	GAG	ATG	TTT	GTG	AAC	GAC	CGT	CTG	GAT	CGA	GAG	GAG	CTG	405
Glu	Thr	Gly	Glu	Met	Phe	Val	Asn	Asp	Arg	Leu	Asp	Arg	Glu	Glu	Leu	
			85					90					95			
TGT	GGG	ACA	CTG	CCC	TCT	TGC	ACT	GTA	ACT	CTG	GAG	TTG	GTA	GTG	GAG	453
Cys	Gly	Thr	Leu	Pro	Ser	Cys	Thr	Val	Thr	Leu	Glu	Leu	Val	Val	Glu	
		100					105					110				
AAC	CCG	CTG	GAG	CTG	TTC	AGC	GTG	GAA	GTG	GTG	ATC	CAG	GAC	ATC	AAC	501
Asn	Pro	Leu	Glu	Leu	Phe	Ser	Val	Glu	Val	Val	Ile	Gln	Asp	Ile	Asn	
	115					120					125					
GAC	AAC	AAT	CCT	GCT	TTC	CCT	ACC	CAG	GAA	ATG	AAA	TTG	GAG	ATT	AGC	549
Asp	Asn	Asn	Pro	Ala	Phe	Pro	Thr	Gln	Glu	Met	Lys	Leu	Glu	Ile	Ser	
130					135					140					145	
GAG	GCC	GTG	GCT	CCG	GGG	ACG	CGC	TTT	CCG	CTC	GAG	AGC	GCG	CAC	GAT	597
Glu	Ala	Val	Ala	Pro	Gly	Thr	Arg	Phe	Pro	Leu	Glu	Ser	Ala	His	Asp	
				150					155					160		
CCC	GAT	CTG	GGA	AGC	AAC	TCT	TTA	CAA	ACC	TAT	GAG	CTG	AGC	CGA	AAT	645
Pro	Asp	Leu	Gly	Ser	Asn	Ser	Leu	Gln	Thr	Tyr	Glu	Leu	Ser	Arg	Asn	
			165					170					175			
GAA	TAC	TTT	GCG	CTT	CGC	GTG	CAG	ACG	CGG	GAG	GAC	AGC	ACC	AAG	TAC	693
Glu	Tyr	Phe	Ala	Leu	Arg	Val	Gln	Thr	Arg	Glu	Asp	Ser	Thr	Lys	Tyr	
		180					185					190				
GCG	GAG	CTG	GTG	TTG	GAG	CGC	GCC	CTG	GAC	CGA	GAA	CGG	GAG	CCT	AGT	741
Ala	Glu	Leu	Val	Leu	Glu	Arg	Ala	Leu	Asp	Arg	Glu	Arg	Glu	Pro	Ser	
	195					200					205					
CTC	CAG	TTA	GTG	CTG	ACG	GCG	TTG	GAC	GGA	GGG	ACC	CCA	GCT	CTC	TCC	789
Leu	Gln	Leu	Val	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Thr	Pro	Ala	Leu	Ser	
210					215					220					225	
GCC	AGC	CTG	CCT	ATT	CAC	ATC	AAG	GTG	CTG	GAC	GCG	AAT	GAC	AAT	GCG	837
Ala	Ser	Leu	Pro	Ile	His	Ile	Lys	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	
			230						235					240		
CCT	GTC	TTC	AAC	CAG	TCC	TTG	TAC	CGG	GCG	CGC	GTT	CCT	GGA	GGA	TGC	885
Pro	Val	Phe	Asn	Gln	Ser	Leu	Tyr	Arg	Ala	Arg	Val	Pro	Gly	Gly	Cys	
			245					250					255			
ACC	TCC	GGC	ACG	CGC	GTG	GTA	CAA	GTC	CTT	GCA	ACG	GAT	CTG	GAT	GAA	933
Thr	Ser	Gly	Thr	Arg	Val	Val	Gln	Val	Leu	Ala	Thr	Asp	Leu	Asp	Glu	
		260					265					270				
GGC	CCC	AAC	GGT	GAA	ATT	ATT	TAC	TCC	TTC	GGC	AGC	CAC	AAC	CGC	GCC	981
Gly	Pro	Asn	Gly	Glu	Ile	Ile	Tyr	Ser	Phe	Gly	Ser	His	Asn	Arg	Ala	
	275					280					285					

GGC Gly 290	GTG Val	CGG Arg	CAA Gln	CTA Leu	TTC Phe 295	GCC Ala	TTA Leu	GAC Asp	CTT Leu 300	GTA Val	ACC Thr	GGG Gly	ATG Met	CTG Leu	ACA Thr 305	1029
ATC Ile	AAG Lys	GGT Gly	CGG Arg	CTG Leu 310	GAC Asp	TTC Phe	GAG Glu	GAC Asp	ACC Thr 315	AAA Lys	CTC Leu	CAT His	GAG Glu	ATT Ile 320	TAC Tyr	1077
ATC Ile	CAG Gln	GCC Ala	AAA Lys 325	GAC Asp	AAG Lys	GGC Gly	GCC Ala	AAT Asn 330	CCC Pro	GAA Glu	GGA Gly	GCA Ala	CAT His 335	TGC Cys	AAA Lys	1125
GTG Val	TTG Leu	GTG Val 340	GAG Glu	GTT Val	GTG Val	GAT Asp	GTG Val 345	AAT Asn	GAC Asp	AAC Asn	GCC Ala	CCG Pro 350	GAG Glu	ATC Ile	ACA Thr	1173
GTC Val 355	ACC Thr	TCC Ser	GTG Val	TAC Tyr	AGC Ser	CCA Pro 360	GTA Val	CCC Pro	GAG Glu	GAT Asp	GCC Ala 365	TCT Ser	GGG Gly	ACT Thr	GTC Val	1221
ATC Ile 370	GCT Ala	TTG Leu	CTC Leu	AGT Ser	GTG Val 375	ACT Thr	GAC Asp	CTG Leu	GAT Asp 380	GCT Ala	GGC Gly	GAG Glu	AAC Asn	GGG Gly	CTG Leu 385	1269
GTG Val	ACC Thr	TGC Cys	GAA Glu	GTT Val 390	CCA Pro	CCG Pro	GGT Gly	CTC Leu	CCT Pro 395	TTC Phe	AGC Ser	CTT Leu	ACT Thr	TCT Ser	TCC Ser 400	1317
CTC Leu	AAG Lys	AAT Asn	TAC Tyr 405	TTC Phe	ACT Thr	TTG Leu	AAA Lys	ACC Thr 410	AGT Ser	GCA Ala	GAC Asp	CTG Leu	GAT Asp 415	CGG Arg	GAG Glu	1365
ACT Thr	GTG Val	CCA Pro 420	GAA Glu	TAC Tyr	AAC Asn	CTC Leu	AGC Ser 425	ATC Ile	ACC Thr	GCC Ala	CGA Arg	GAC Asp 430	GCC Ala	GGA Gly	ACC Thr	1413
CCT Pro 435	TCC Ser	CTC Leu	TCA Ser	GCC Ala	CTT Leu	ACA Thr 440	ATA Ile	GTG Val	CGT Arg	GTT Val	CAA Gln 445	GTG Val	TCC Ser	GAC Asp	ATC Ile	1461
AAT Asn 450	GAC Asp	AAC Asn	CCT Pro	CCA Pro	CAA Gln 455	TCT Ser	TCT Ser	CAA Gln	TCT Ser 460	TCC Ser	TAC Tyr	GAC Asp	GTT Val	TAC Tyr	ATT Ile 465	1509
GAA Glu	GAA Glu	AAC Asn	AAC Asn	CTC Leu 470	CCC Pro	GGG Gly	GCT Ala	CCA Pro	ATA Ile 475	CTA Leu	AAC Asn	CTA Leu	AGT Ser	GTC Val	TGG Trp 480	1557
GAC Asp	CCC Pro	GAC Asp	GCC Ala 485	CCG Pro	CAG Gln	AAT Asn	GCT Ala	CGG Arg 490	CTT Leu	TCT Ser	TTC Phe	TTT Phe	CTC Leu 495	TTG Leu	GAG Glu	1605
CAA Gln	GGA Gly	GCT Ala	GAA Glu	ACC Thr	GGG Gly	CTA Leu	GTG Val 505	GGT Gly	CGC Arg	TAT Tyr	TTC Phe	ACA Thr 510	ATA Ile	AAT Asn	CGT Arg	1653
GAC Asp 515	AAT Asn	GGC Gly	ATA Ile	GTG Val	TCA Ser	TCC Ser 520	TTA Leu	GTG Val	CCC Pro	CTA Leu	GAC Asp 525	TAT Tyr	GAG Glu	GAT Asp	CGG Arg	1701

CGG Arg 530	GAA Glu	TTT Phe	GAA Glu	TTA Leu	ACA Thr 535	GCT Ala	CAT His	ATC Ile	AGC Ser	GAT Asp 540	GGG Gly	GGC Gly	ACC Thr	CCG Pro	GTC Val 545	1749
CTA Leu	GCC Ala	ACC Thr	AAC Asn	ATC Ile 550	AGC Ser	GTG Val	AAC Asn	ATA Ile	TTT Phe 555	GTC Val	ACT Thr	GAT Asp	CGC Arg	AAT Asn 560	GAC Asp	1797
AAT Asn	GCC Ala	CCC Pro	CAG Gln 565	GTC Val	CTA Leu	TAT Tyr	CCT Pro	CGG Arg 570	CCA Pro	GGT Gly	GGG Gly	AGC Ser	TCG Ser 575	GTG Val	GAG Glu	1845
ATG Met	CTG Leu	CCT Pro 580	CGA Arg	GGT Gly	ACC Thr	TCA Ser	GCT Ala 585	GGC Gly	CAC His	CTA Leu	GTG Val	TCA Ser	CGG Arg 590	GTG Val	GTA Val	1893
GGC Gly	TGG Trp 595	GAC Asp	GCG Ala	GAT Asp	GCA Ala	GGG Gly 600	CAC His	AAT Asn	GCC Ala	TGG Trp	CTC Leu 605	TCC Ser	TAC Tyr	AGT Ser	CTC Leu	1941
TTT Phe 610	GGA Gly	TCC Ser	CCT Pro	AAC Asn	CAG Gln 615	AGC Ser	CTT Leu	TTT Phe	GCC Ala 620	ATA Ile	GGG Gly	CTG Leu	CAC His	ACT Thr	GGT Gly 625	1989
CAA Gln	ATC Ile	AGT Ser	ACT Thr	GCC Ala 630	CGT Arg	CCA Pro	GTC Val	CAA Gln	GAC Asp 635	ACA Thr	GAT Asp	TCA Ser	CCC Pro	AGG Arg 640	CAG Gln	2037
ACT Thr	CTC Leu	ACT Thr	GTC Val 645	TTG Leu	ATC Ile	AAA Lys	GAC Asp	AAT Asn 650	GGG Gly	GAG Glu	CCT Pro	TCG Ser	CTC Leu 655	TCC Ser	ACC Thr	2085
ACT Thr	GCT Ala	ACC Thr 660	CTC Leu	ACT Thr	GTG Val	TCA Ser	GTA Val 665	ACC Thr	GAG Glu	GAC Asp	TCT Ser	CCT Pro	GAA Glu 670	GCC Ala	CGA Arg	2133
GCC Ala	GAG Glu 675	TTC Phe	CCC Pro	TCT Ser	GGC Gly	TCT Ser 680	GCC Ala	CCC Pro	CGG Arg	GAG Glu	CAG Gln 685	AAA Lys	AAA Lys	AAT Asn	CTC Leu	2181
ACC Thr 690	TTT Phe	TAT Tyr	CTA Leu	CTT Leu	CTT Leu 695	TCT Ser	CTA Leu	ATC Ile	CTG Leu	GTT Val 700	TCT Ser	GTG Val	GGC Gly	TTC Phe	GTG Val 705	2229
GTC Val	ACA Thr	GTG Val	TTC Phe	GGA Gly 710	GTA Val	ATC Ile	ATA Ile	TTC Phe	AAA Lys 715	GTT Val	TAC Tyr	AAG Lys	TGG Trp 720	AAG Lys	CAG Gln	2277
TCT Ser	AGA Arg	GAC Asp	CTA Leu 725	TAC Tyr	CGA Arg	GCC Ala	CCG Pro	GTG Val 730	AGC Ser	TCA Ser	CTG Leu	TAC Tyr	CGA Arg 735	ACA Thr	CCA Pro	2325
GGG Gly	CCC Pro	TCC Ser 740	TTG Leu	CAC His	GCG Ala	GAC Asp	GCC Ala 745	GTG Val	CGG Arg	GGA Gly	GGC Gly	CTG Leu 750	ATG Met	TCG Ser	CCG Pro	2373
CAC His 755	CTT Leu	TAC Tyr	CAT His	CAG Gln	GTG Val	TAT Tyr 760	CTC Leu	ACC Thr	ACG Thr	GAC Asp	TCC Ser 765	CGC Arg	CGC Arg	AGC Ser	GAC Asp	2421

CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln 770 775 780 785	2469
AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly 790 795 800	2517
GCA GAG AGC GCC CCT CCC GGA CAG CAA GCC CCG CCC AAC ACG GAC TGG Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp Trp 805 810 815	2565
CGT TTC TCT CAG GCC CAG AGA CCC GGC ACC AGC GGC TCC CAA AAT GGC Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Gln Asn Gly 820 825 830	2613
GAT GAC ACC GGC ACC TGG CCC AAC AAC CAG TTT GAC ACA GAG ATG CTG Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met Leu 835 840 845	2661
CAA GCC ATG ATC TTG GCG TCC GCC AGT GAA GCT GCT GAT GGG AGC TCC Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser Ser 850 855 860 865	2709
ACC CTG GGA GGG GGT GCC GGC ACC ATG GGA TTG AGC GCC CGC TAC GGA Thr Leu Gly Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr Gly 870 875 880	2757
CCC CAG TTC ACC CTG CAG CAC GTG CCC GAC TAC CGC CAG AAT GTC TAC Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val Tyr 885 890 895	2805
ATC CCA GGC AGC AAT GCA CAC T GACCAACGCA GCTGGCAAGC GGATGGCAAG Ile Pro Gly Ser Asn Ala His 900	2857
CCCCAGCAGG TGGCAATGGC AACAAGAAGA AGTCGGCAAG AAGGAGAAGA AGTAACATGG	2917
AGGCCAGGCC AAGAGCCACA GGGCAGCCTC TCCCCGAACC AGCCCAGCTT CTCCTTACCT	2977
GCACCCAGGC CTCAGAGTTT CAGGGCTAAC CCCCAGAATA CTGGTAGGGG CCAAGGCATC	3037
TCCCTTGGA ACAGAAACAA GTGCCATCAC ACCATCCCTT CCCCAGGTGT AATATCCAAA	3097
GCAGTTCCGC TGGGAACCCC ATCCAATCAG TGGCTGTACC CATTTGGGTA GTGGGGTTCA	3157
TGTAGACACC AAGAACCATT TGCCACACCC CGTTTAGTTA CAGCTGAACC CTCCATCTTC	3217
CAAATCAATC AGGCCCATCC ATCCCATGCC TCCCTCCTCC CCACCCCACT CCAACAGTTC	3277
CTCTTTCCCG AGTAAGGTGG TTGGGGTGTT GAAGTACCAA GTAACCTACA AGCCTCCTAG	3337
TTCTGAAAAG TTGGAAGGGC ATCATGACCT CTGGCCTCT CCTTTGATTC TCAATCTTCC	3397
CCCAAAGCAT GGTTTGGTGC CAGCCCCTTC ACCTCCTTCC AGAGCCCAAG ATCAATGCTC	3457
AAGTTTTGGA GGACATGATC ACCATCCCCA TGGTACTGAT GCTTGCTGGA TTTAGGGAGG	3517
GCATTTTGCT ACCAAGCCTC TTCCCAACGC CCTGGGACCA GTCTTCTGTT TTGTTTTTCA	3577
TTGTTTGAGC TTTCCACTGC ATGCCTTGAC TTCCCCCACC TCCTCCTCAA ACAAGAGACT	3637

CCACTGCATG TTCCAAGACA GTATGGGGTG GTAAGATAAG GAAGGGAAGT GTGTGGATGT	3697
GGATGGTGGG GGCATGGACA AAGCTTGACA CATCAAGTTA TCAAGGCCTT GGAGGAGGCT	3757
CTGTATGTCC TCAGGGGACT GACAACATCC TCCAGATTCC AGCCATAAAC CAATAACTAG	3817
GCTGGACCCT TCCCACTACA TAATAGGGCT CAGCCAGGCA GCCAGCTTTG GGCTGAGCTA	3877
ACAGGACCAA TGGATTAACT GGCATTTTCAG TCCAAGGAAG CTCGAAGCAG GTTTAGGACC	3937
AGGTCCCCCTT GAGAGGTCAG AGGGGCCTCT GTGGGTGCTG GGTACTCCAG AGGTGCCACT	3997
GGTGAAGGG TCAGCGGAGC CCCAGCAGGA AGGGTGGGCC AGCCAGGCCA TTCTTAGTCC	4057
CTGGGTGGG GAGGCAGGA GCTAGGGCAG GGACCAAATG AACAGAAAGT CTCAGCCCAG	4117
GATGGGGCTT CTTCAACAGG CCCCTGCCCT CCTGAAGCCT CAGTCCTTCA CCTTGCCAGG	4177
TGCCGTTTCT CTTCCGTGAA GGCCACTGCC CAGGTCCCCA GTGCGCCCCC TAGTGGCCAT	4237
AGCCTGGTTA AAGTTCCCCA GTGCCTCCTT GTGATAGACC TTCTTCTCCC ACCCCCTTCT	4297
GCCCCTGGGT CCCCGGCCAT CCAGCGGGGC TGCCAGAGAA CCCAGACCT GCCCTTACAG	4357
TAGTGTAGCG CCCCTCCCT CTTTCGGCTG GTGTAGAATA GCCAGTAGTG TAGTGCGGTG	4417
TGCTTTTACG TGATGGCGGG TGGGCAGCGG GCGGCGGCGT CCGCGCAGCC GTCTGTCTT	4477
GATCTGCCCC CGGCGGCCCC TGTGTGTGTT TGTGCTGTGT CCAGCGCTAA GGCGACCCCC	4537
TCCCCCGTAC TGACTTCTCC TATAAGCGCT TCTCTTCGCA TAGTCACGTA GCTCCCACCC	4597
CACCCTCTTC CTGTGTCTCA CGCAAGTTT ATACTCTAAT ATTTATATGG CTTTTTTTCT	4657
TCGACAAAAA AATAATAAAA CGTTTCTTCT GAAAAAAAAA AAAAAAAA	4705

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val	
1 5 10 15	
Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val	
20 25 30	
Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly	
35 40 45	
Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg	
50 55 60	

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
65 70 75 80

Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
85 90 95

Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
100 105 110

Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
260 265 270

Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
275 280 285

Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
290 295 300

Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
305 310 315 320

Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
325 330 335

Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
340 345 350

Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
355 360 365

Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
370 375 380

Leu	Val	Thr	Cys	Glu	Val	Pro	Pro	Gly	Leu	Pro	Phe	Ser	Leu	Thr	Ser	385	390	395	400
Ser	Leu	Lys	Asn	Tyr	Phe	Thr	Leu	Lys	Thr	Ser	Ala	Asp	Leu	Asp	Arg	405	410	415	
Glu	Thr	Val	Pro	Glu	Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Gly	420	425	430	
Thr	Pro	Ser	Leu	Ser	Ala	Leu	Thr	Ile	Val	Arg	Val	Gln	Val	Ser	Asp	435	440	445	
Ile	Asn	Asp	Asn	Pro	Pro	Gln	Ser	Ser	Gln	Ser	Ser	Tyr	Asp	Val	Tyr	450	455	460	
Ile	Glu	Glu	Asn	Asn	Leu	Pro	Gly	Ala	Pro	Ile	Leu	Asn	Leu	Ser	Val	465	470	475	480
Trp	Asp	Pro	Asp	Ala	Pro	Gln	Asn	Ala	Arg	Leu	Ser	Phe	Phe	Leu	Leu	485	490	495	
Glu	Gln	Gly	Ala	Glu	Thr	Gly	Leu	Val	Gly	Arg	Tyr	Phe	Thr	Ile	Asn	500	505	510	
Arg	Asp	Asn	Gly	Ile	Val	Ser	Ser	Leu	Val	Pro	Leu	Asp	Tyr	Glu	Asp	515	520	525	
Arg	Arg	Glu	Phe	Glu	Leu	Thr	Ala	His	Ile	Ser	Asp	Gly	Gly	Thr	Pro	530	535	540	
Val	Leu	Ala	Thr	Asn	Ile	Ser	Val	Asn	Ile	Phe	Val	Thr	Asp	Arg	Asn	545	550	555	560
Asp	Asn	Ala	Pro	Gln	Val	Leu	Tyr	Pro	Arg	Pro	Gly	Gly	Ser	Ser	Val	565	570	575	
Glu	Met	Leu	Pro	Arg	Gly	Thr	Ser	Ala	Gly	His	Leu	Val	Ser	Arg	Val	580	585	590	
Val	Gly	Trp	Asp	Ala	Asp	Ala	Gly	His	Asn	Ala	Trp	Leu	Ser	Tyr	Ser	595	600	605	
Leu	Phe	Gly	Ser	Pro	Asn	Gln	Ser	Leu	Phe	Ala	Ile	Gly	Leu	His	Thr	610	615	620	
Gly	Gln	Ile	Ser	Thr	Ala	Arg	Pro	Val	Gln	Asp	Thr	Asp	Ser	Pro	Arg	625	630	635	640
Gln	Thr	Leu	Thr	Val	Leu	Ile	Lys	Asp	Asn	Gly	Glu	Pro	Ser	Leu	Ser	645	650	655	
Thr	Thr	Ala	Thr	Leu	Thr	Val	Ser	Val	Thr	Glu	Asp	Ser	Pro	Glu	Ala	660	665	670	
Arg	Ala	Glu	Phe	Pro	Ser	Gly	Ser	Ala	Pro	Arg	Glu	Gln	Lys	Lys	Asn	675	680	685	
Leu	Thr	Phe	Tyr	Leu	Leu	Leu	Ser	Leu	Ile	Leu	Val	Ser	Val	Gly	Phe	690	695	700	

Val Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys
705 710 715 720

Gln Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr
725 730 735

Pro Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser
740 745 750

Pro His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser
755 760 765

Asp Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg
770 775 780

Gln Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu
785 790 795 800

Gly Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp
805 810 815

Trp Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Ser Gln Asn
820 825 830

Gly Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met
835 840 845

Leu Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser
850 855 860

Ser Thr Leu Gly Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr
865 870 875 880

Gly Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val
885 890 895

Tyr Ile Pro Gly Ser Asn Ala His
900

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Asp Trp Val Ile Pro Pro Ile Asn Leu Pro Glu Asn Ser Arg Gly Pro
1 5 10 15

Phe Pro Gln Glu Leu Val Arg Ile Arg Ser Asp Arg Asp Lys Asn Leu
20 25 30

Ser Leu Arg Tyr Thr Val Thr Gly Pro Gly Ala Asp Gln Pro Pro Thr
35 40 45

Gly Ile Phe Ile Ile Asn Pro Ile Ser Gly Gln Leu Ser Val Thr Lys
50 55 60

Pro Leu Asp Arg Glu Gln Ile Ala Arg Phe His Leu Arg Ala His Ala
65 70 75 80

Val Asp Ile Asn Gly Asn Gln Val Glu Asn Pro Ile Asp Ile Val Ile
85 90 95

Asn Val Ile Asp Met Asn Asp Asn Arg Pro Glu Phe Leu His Gln Val
100 105 110

Trp Asn Gly Ser Val Pro Glu Gly Ser Lys Pro Gly Thr Tyr Val Met
115 120 125

Thr Val Thr Ala Ile Asp Ala Asp Asp Pro Asn Ala Leu Asn Gly Met
130 135 140

Leu Arg Tyr Arg Ile Leu Ser Gln Ala Pro Ser Thr Pro Ser Pro Asn
145 150 155 160

Met Phe Thr Ile Asn Asn Glu Thr Gly Asp Ile Ile Thr Val Ala Ala
165 170 175

Gly Leu Asp Arg Glu Lys Val Gln Gln Tyr Thr Leu Ile Ile Gln Ala
180 185 190

Thr Asp Met Glu Gly Asn Pro Thr Tyr Gly Leu Ser Asn Thr Ala Thr
195 200 205

Ala Val Ile Thr Val Thr Asp Val Asn Asp Asn Pro Pro Glu Phe Thr
210 215 220

Ala Met Thr Phe Tyr Gly Glu Val Pro Glu Asn Arg Val Asp Ile Ile
225 230 235 240

Val Ala Asn Leu Thr Val Thr Asp Lys Asp Gln Pro His Thr Pro Ala
245 250 255

Trp Asn Ala Val Thr Arg Ile Ser Gly Gly Asp Pro Thr Gly Arg Phe
260 265 270

Ala Ile Gln Thr Asp Pro Asn Ser Asn Asp Gly Leu Val Thr Val Val
275 280 285

Lys Pro Ile Asp Phe Glu Thr Asn Arg Met Phe Val Leu Thr Val Ala
290 295 300

Ala Glu Asn Gln Val Pro Leu Ala Lys Gly Ile Gln His Pro Pro Gln
305 310 315 320

Ser Thr Ala Thr Val Ser Val Thr Val Ile Asp Val Asn Glu Asn Pro
325 330 335

Tyr Phe Ala Pro Asn Pro Lys Ile Ile Arg Gln Glu Glu Gly Leu His
340 345 350

Ala Gly Thr Met Leu Thr Thr Phe Thr Ala Gly Asp Pro Asp Arg Tyr
355 360 365

Met Gln Gln Asn Ile Arg Tyr Thr Lys Leu Ser Asp Pro Ala Asn Trp
370 375 380

Leu Lys Ile Asp Pro Val Asn Gly Gln Ile Thr Thr Ile Ala Val Leu
385 390 395 400

Asp Arg Glu Ser Pro Asn Val Lys Asn Asn Ile Tyr Asn Ala Thr Phe
405 410 415

/ Leu Ala Ser Asp Asn Gly Ile Pro Pro Met Ser Gly Thr Gly Thr Leu
420 425 430

Gln Ile Tyr Leu Leu Asp Ile Asn Asp Asn Ala Pro Gln Val Leu Pro
435 440 445

Gln Glu Ala Glu Thr Cys Glu Thr Pro Asp Pro Asn Ser Ile Asn Ile
450 455 460

Thr Thr Ala Leu Asp Tyr Asp Ile Asp Pro Asn Ala Gly Pro Phe Ala
465 470 475 480

Tyr Asp Leu Pro Leu Ser Pro Val Thr Ile Lys Arg Asn Trp Thr Ile
485 490 495

Thr Arg Leu Asn Gly Asp Phe Ala Gln Leu Asn Leu Lys Ile Lys Phe
500 505 510

Leu Glu Ala Gly Ile Tyr Glu Val Pro Ile Ile Ile Thr Asp Ser Gly
515 520 525

Asn Pro Pro Lys Ser Asn Lys Ser Ile Leu Arg Val Arg Val Cys Gln
530 535 540

Cys Asp Phe Asn Gly Asp Cys Thr Asp Val Asp Arg
545 550 555

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Glu Asp Thr Val Tyr Ser Phe Asp Ile Pro Glu Asn Ala Gln Arg Gly
1 5 10 15

Tyr Gln Val Gly Gln Ile Val Ala Arg Asp Ala Asp Leu Gly Gln Asn
20 25 30

Ala Gln Leu Ser Tyr Gly Val Val Ser Asp Trp Ala Asn Asp Val Phe
35 40 45

Ser Leu Asn Pro Gln Thr Gly Met Leu Thr Leu Thr Ala Arg Leu Asp
50 55 60
Tyr Glu Glu Val Gln His Tyr Ile Leu Ile Val Gln Ala Gln Asp Asn
65 70 75 80
Gly Gln Pro Ser Leu Ser Thr Thr Ile Thr Val Tyr Cys Asn Val Leu
85 90 95
Asp Leu Asn Asp Asn Ala Pro Ile Phe
100 105

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asp Xaa Asp Xaa Gly Xaa Asn
1 5

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ala Xaa Asp Xaa Gly Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 495..4103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCTCTATTTCG ACATTCTCTT TGGATTGTTT TGCTATAACT TGAAATTTGG GATGTCACAA	60
ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTTCTGCT AATCTCCCAG GCTGGCAGCA	120
TTGGAGACTT GCTGACTTCT TTCATCCCCC ACTCTTTTCA CCTGAAATTC CTTTCCTTGG	180
TTTTGCTCTA AGTCCTATGC TTCAGTCAGG GGCCAACCAA ATCTCACTGC CTCCTTTTTA	240
TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT	300
ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCACT	360
CGTTTTTCGTA CCTCTTCATG GTGATGGGGA GCCCTTTGGA GGTGGTGA CTGCTTTATA	420
CTCCTCATGA TGCTTCACAT GTGGCAGGCG TGGAGTGCCC GGAGGCGGCC CTCCTGATTC	480
TGGGGCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG	530
Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly	
1 5 10	
CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG	578
Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Leu	
15 20 25	
GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG	626
Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu	
30 35 40	
GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT	674
Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly	
45 50 55 60	
TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC	722
Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr	
65 70 75	
CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC	770
Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser	
80 85 90	
ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT	818
Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp	
95 100 105	
CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT	866
Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn	
110 115 120	
GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT	914
Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn	
125 130 135 140	
GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT	962
Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro	
145 150 155	
GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC	1010
Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp	
160 165 170	

CGT	GAT	GCT	GGT	CCC	AAC	GGT	GTG	GCA	TCC	TAT	GAG	CTG	CAG	GTG	GCA	1058
Arg	Asp	Ala	Gly	Pro	Asn	Gly	Val	Ala	Ser	Tyr	Glu	Leu	Gln	Val	Ala	
		175					180					185				
GAG	GAC	CAG	GAG	GAG	AAG	CAA	CCA	CAG	CTC	ATT	GTG	ATG	GGC	AAC	CTG	1106
Glu	Asp	Gln	Glu	Glu	Lys	Gln	Pro	Gln	Leu	Ile	Val	Met	Gly	Asn	Leu	
	190					195					200					
GAC	CGT	GAG	CGC	TGG	GAC	TCC	TAT	GAC	CTC	ACC	ATC	AAG	GTG	CAG	GAT	1154
Asp	Arg	Glu	Arg	Trp	Asp	Ser	Tyr	Asp	Leu	Thr	Ile	Lys	Val	Gln	Asp	
205					210					215					220	
GGC	GGC	AGC	CCC	CCA	CGC	GCC	ACG	AGT	GCC	CTG	CTG	CGT	GTC	ACC	GTG	1202
Gly	Gly	Ser	Pro	Pro	Arg	Ala	Thr	Ser	Ala	Leu	Leu	Arg	Val	Thr	Val	
				225					230					235		
CTT	GAC	ACC	AAT	GAC	AAC	GCC	CCC	AAG	TTT	GAG	CGG	CCC	TCC	TAT	GAG	1250
Leu	Asp	Thr	Asn	Asp	Asn	Ala	Pro	Lys	Phe	Glu	Arg	Pro	Ser	Tyr	Glu	
			240					245					250			
GCC	GAA	CTA	TCT	GAG	AAT	AGC	CCC	ATA	GGC	CAC	TCG	GTC	ATC	CAG	GTG	1298
Ala	Glu	Leu	Ser	Glu	Asn	Ser	Pro	Ile	Gly	His	Ser	Val	Ile	Gln	Val	
	255						260					265				
AAG	GCC	AAT	GAC	TCA	GAC	CAA	GGT	GCC	AAT	GCA	GAA	ATC	GAA	TAC	ACA	1346
Lys	Ala	Asn	Asp	Ser	Asp	Gln	Gly	Ala	Asn	Ala	Glu	Ile	Glu	Tyr	Thr	
	270					275					280					
TTC	CAC	CAG	GCG	CCC	GAA	GTT	GTG	AGG	CGT	CTT	CTT	CGA	CTG	GAC	AGG	1394
Phe	His	Gln	Ala	Pro	Glu	Val	Val	Arg	Arg	Leu	Leu	Arg	Leu	Asp	Arg	
285					290					295					300	
AAC	ACT	GGA	CTT	ATC	ACT	GTT	CAG	GGC	CCG	GTG	GAC	CGT	GAG	GAC	CTA	1442
Asn	Thr	Gly	Leu	Ile	Thr	Val	Gln	Gly	Pro	Val	Asp	Arg	Glu	Asp	Leu	
				305					310					315		
AGC	ACC	CTG	CGC	TTC	TCA	GTG	CTT	GCT	AAG	GAC	CGA	GGC	ACC	AAC	CCC	1490
Ser	Thr	Leu	Arg	Phe	Ser	Val	Leu	Ala	Lys	Asp	Arg	Gly	Thr	Asn	Pro	
			320					325					330			
AAG	AGT	GCC	CGT	GCC	CAG	GTG	GTT	GTG	ACC	GTG	AAG	GAC	ATG	AAT	GAC	1538
Lys	Ser	Ala	Arg	Ala	Gln	Val	Val	Val	Thr	Val	Lys	Asp	Met	Asn	Asp	
		335				340						345				
AAT	GCC	CCC	ACC	ATT	GAG	ATC	CGG	GGC	ATA	GGG	CTA	GTG	ACT	CAT	CAA	1586
Asn	Ala	Pro	Thr	Ile	Glu	Ile	Arg	Gly	Ile	Gly	Leu	Val	Thr	His	Gln	
	350					355					360					
GAT	GGG	ATG	GCT	AAC	ATC	TCA	GAG	GAT	GTG	GCA	GAG	GAG	ACA	GCT	GTG	1634
Asp	Gly	Met	Ala	Asn	Ile	Ser	Glu	Asp	Val	Ala	Glu	Glu	Thr	Ala	Val	
365					370					375					380	
GCC	CTG	GTG	CAG	GTG	TCT	GAC	CGA	GAT	GAG	GGA	GAG	AAT	GCA	GCT	GTC	1682
Ala	Leu	Val	Gln	Val	Ser	Asp	Arg	Asp	Glu	Gly	Glu	Asn	Ala	Ala	Val	
				385					390					395		
ACC	TGT	GTG	GTG	GCA	GGT	GAT	GTG	CCC	TTC	CAG	CTG	CGC	CAG	GCC	AGT	1730
Thr	Cys	Val	Val	Ala	Gly	Asp	Val	Pro	Phe	Gln	Leu	Arg	Gln	Ala	Ser	
			400					405						410		

GAG Glu	ACA Thr	GGC Gly	AGT Ser	GAC Asp	AGC Ser	AAG Lys	AAG Lys	AAG Lys	TAT Tyr	TTC Phe	CTG Leu	CAG Gln	ACT Thr	ACC Thr	ACC Thr	1778
		415					420					425				
CCG Pro	CTA Leu	GAC Asp	TAC Tyr	GAG Glu	AAG Lys	GTC Val	AAA Lys	GAC Asp	TAC Tyr	ACC Thr	ATT Ile	GAG Glu	ATT Ile	GTG Val	GCT Ala	1826
	430					435					440					
GTG Val	GAC Asp	TCT Ser	GGC Gly	AAC Asn	CCC Pro	CCA Pro	CTC Leu	TCC Ser	AGC Ser	ACT Thr	AAC Asn	TCC Ser	CTC Leu	AAG Lys	GTG Val	1874
	445				450					455					460	
CAG Gln	GTG Val	GTG Val	GAC Asp	GTC Val	AAT Asn	GAC Asp	AAC Asn	GCA Ala	CCT Pro	GTC Val	TTC Phe	ACT Thr	CAG Gln	AGT Ser	GTC Val	1922
				465					470					475		
ACT Thr	GAG Glu	GTC Val	GCC Ala	TTC Phe	CCG Pro	GAA Glu	AAC Asn	AAC Asn	AAG Lys	CCT Pro	GGT Gly	GAA Glu	GTG Val	ATT Ile	GCT Ala	1970
			480					485					490			
GAG Glu	ATC Ile	ACT Thr	GCC Ala	AGT Ser	GAT Asp	GCT Ala	GAC Asp	TCT Ser	GGC Gly	TCT Ser	AAT Asn	GCT Ala	GAG Glu	CTG Leu	GTT Val	2018
		495					500					505				
TAC Tyr	TCT Ser	CTG Leu	GAG Glu	CCT Pro	GAG Glu	CCG Pro	GCT Ala	GCT Ala	AAG Lys	GGC Gly	CTC Leu	TTC Phe	ACC Thr	ATC Ile	TCA Ser	2066
	510					515					520					
CCC Pro	GAG Glu	ACT Thr	GGA Gly	GAG Glu	ATC Ile	CAG Gln	GTG Val	AAG Lys	ACA Thr	TCT Ser	CTG Leu	GAT Asp	CGG Arg	GAA Glu	CAG Gln	2114
	525				530					535					540	
CGG Arg	GAG Glu	AGC Ser	TAT Tyr	GAG Glu	TTG Leu	AAG Lys	GTG Val	GTG Val	GCA Ala	GCT Ala	GAC Asp	CGG Arg	GGC Gly	AGT Ser	CCT Pro	2162
				545					550					555		
AGC Ser	CTC Leu	CAG Gln	GGC Gly	ACA Thr	GCC Ala	ACT Thr	GTC Val	CTT Leu	GTC Val	AAT Asn	GTG Val	CTG Leu	GAC Asp	TGC Cys	AAT Asn	2210
			560					565					570			
GAC Asp	AAT Asn	GAC Asp	CCC Pro	AAA Lys	TTT Phe	ATG Met	CTG Leu	AGT Ser	GGC Gly	TAC Tyr	AAC Asn	TTC Phe	TCA Ser	GTG Val	ATG Met	2258
		575					580					585				
GAG Glu	AAC Asn	ATG Met	CCA Pro	GCA Ala	CTG Leu	AGT Ser	CCA Pro	GTG Val	GGC Gly	ATG Met	GTG Val	ACT Thr	GTC Val	ATT Ile	GAT Asp	2306
	590					595					600					
GGA Gly	GAC Asp	AAG Lys	GGG Gly	GAG Glu	AAT Asn	GCC Ala	CAG Gln	GTG Val	CAG Gln	CTC Leu	TCA Ser	GTG Val	GAG Glu	CAG Gln	GAC Asp	2354
	605				610					615					620	
AAC Asn	GGT Gly	GAC Asp	TTT Phe	GTT Val	ATC Ile	CAG Gln	AAT Asn	GGC Gly	ACA Thr	GGC Gly	ACC Thr	ATC Ile	CTA Leu	TCC Ser	AGC Ser	2402
				625					630					635		
CTG Leu	AGC Ser	TTT Phe	GAT Asp	CGA Arg	GAG Glu	CAA Gln	CAA Gln	AGC Ser	ACC Thr	TAC Tyr	ACC Thr	TTC Phe	CAG Gln	CTG Leu	AAG Lys	2450
			640					645					650			

GCA	GTG	GAT	GGT	GGC	GTC	CCA	CCT	CGC	TCA	GCT	TAC	GTT	GGT	GTC	ACC	2498
Ala	Val	Asp	Gly	Gly	Val	Pro	Pro	Arg	Ser	Ala	Tyr	Val	Gly	Val	Thr	
	655						660					665				
ATC	AAT	GTG	CTG	GAC	GAG	AAT	GAC	AAC	GCA	CCC	TAT	ATC	ACT	GCC	CCT	2546
Ile	Asn	Val	Leu	Asp	Glu	Asn	Asp	Asn	Ala	Pro	Tyr	Ile	Thr	Ala	Pro	
	670					675					680					
TCT	AAC	ACC	TCT	CAC	AAG	CTG	CTG	ACC	CCC	CAG	ACA	CGT	CTT	GGT	GAG	2594
Ser	Asn	Thr	Ser	His	Lys	Leu	Leu	Thr	Pro	Gln	Thr	Arg	Leu	Gly	Glu	
	685				690					695					700	
ACG	GTC	AGC	CAG	GTG	GCA	GCC	GAG	GAC	TTT	GAC	TCT	GGT	GTC	AAT	GCC	2642
Thr	Val	Ser	Gln	Val	Ala	Ala	Glu	Asp	Phe	Asp	Ser	Gly	Val	Asn	Ala	
				705					710					715		
GAG	CTG	ATC	TAC	AGC	ATT	GCA	GGT	GGC	AAC	CCT	TAT	GGA	CTC	TTC	CAG	2690
Glu	Leu	Ile	Tyr	Ser	Ile	Ala	Gly	Gly	Asn	Pro	Tyr	Gly	Leu	Phe	Gln	
			720					725					730			
ATT	GGG	TCA	CAT	TCA	GGT	GCC	ATC	ACC	CTG	GAG	AAG	GAG	ATT	GAG	CGG	2738
Ile	Gly	Ser	His	Ser	Gly	Ala	Ile	Thr	Leu	Glu	Lys	Glu	Ile	Glu	Arg	
	735					740					745					
CGC	CAC	CAT	GGG	CTA	CAC	CGC	CTG	GTG	GTG	AAG	GTC	AGT	GAC	CGC	GGC	2786
Arg	His	His	Gly	Leu	His	Arg	Leu	Val	Val	Lys	Val	Ser	Asp	Arg	Gly	
	750					755					760					
AAG	CCC	CCA	CGC	TAT	GGC	ACA	GCC	TTG	GTC	CAT	CTT	TAT	GTC	AAT	GAG	2834
Lys	Pro	Pro	Arg	Tyr	Gly	Thr	Ala	Leu	Val	His	Leu	Tyr	Val	Asn	Glu	
	765				770					775					780	
ACT	CTG	GCC	AAC	CGC	ACG	CTG	CTG	GAG	ACC	CTC	CTG	GGC	CAC	AGC	CTG	2882
Thr	Leu	Ala	Asn	Arg	Thr	Leu	Leu	Glu	Thr	Leu	Leu	Gly	His	Ser	Leu	
				785					790					795		
GAC	ACG	CCG	CTG	GAT	ATT	GAC	ATT	GCT	GGG	GAT	CCA	GAA	TAT	GAG	CGC	2930
Asp	Thr	Pro	Leu	Asp	Ile	Asp	Ile	Ala	Gly	Asp	Pro	Glu	Tyr	Glu	Arg	
			800					805					810			
TCC	AAG	CAG	CGT	GGC	AAC	ATT	CTC	TTT	GGT	GTG	GTG	GCT	GGT	GTG	GTG	2978
Ser	Lys	Gln	Arg	Gly	Asn	Ile	Leu	Phe	Gly	Val	Val	Ala	Gly	Val	Val	
	815						820					825				
GCC	GTG	GCC	TTG	CTC	ATC	GCC	CTG	GCG	GTT	CTT	GTG	CGC	TAC	TGC	AGA	3026
Ala	Val	Ala	Leu	Leu	Ile	Ala	Leu	Ala	Val	Leu	Val	Arg	Tyr	Cys	Arg	
	830					835					840					
CAG	CGG	GAG	GCC	AAA	AGT	GGT	TAC	CAG	GCT	GGT	AAG	AAG	GAG	ACC	AAG	3074
Gln	Arg	Glu	Ala	Lys	Ser	Gly	Tyr	Gln	Ala	Gly	Lys	Lys	Glu	Thr	Lys	
	845				850					855					860	
GAC	CTG	TAT	GCC	CCC	AAG	CCC	AGT	GGC	AAG	GCC	TCC	AAG	GGA	AAC	AAA	3122
Asp	Leu	Tyr	Ala	Pro	Lys	Pro	Ser	Gly	Lys	Ala	Ser	Lys	Gly	Asn	Lys	
			865					870						875		
AGC	AAA	GGC	AAG	AAG	AGC	AAG	TCC	CCA	AAG	CCC	GTG	AAG	CCA	GTG	GAG	3170
Ser	Lys	Gly	Lys	Lys	Ser	Lys	Ser	Pro	Lys	Pro	Val	Lys	Pro	Val	Glu	
			880					885					890			

GAC Asp	GAG Glu	GAT Asp	GAG Glu	GCC Ala	GGG Gly	CTG Leu	CAG Gln	AAG Lys	TCC Ser	CTC Leu	AAG Lys	TTC Phe	AAC Asn	CTG Leu	ATG Met	3218
895 900 905																
AGC Ser	GAT Asp	GCC Ala	CCT Pro	GGG Gly	GAC Asp	AGT Ser	CCC Pro	CGC Arg	ATC Ile	CAC His	CTG Leu	CCC Pro	CTC Leu	AAC Asn	TAC Tyr	3266
910 915 920																
CCA Pro	CCA Pro	GGC Gly	AGC Ser	CCT Pro	GAC Asp	CTG Leu	GGC Gly	CGC Arg	CAC His	TAT Tyr	CGC Arg	TCT Ser	AAC Asn	TCC Ser	CCA Pro	3314
925 930 935 940																
CTG Leu	CCT Pro	TCC Ser	ATC Ile	CAG Gln	CTG Leu	CAG Gln	CCC Pro	CAG Gln	TCA Ser	CCC Pro	TCA Ser	GCC Ala	TCC Ser	AAG Lys	AAG Lys	3362
945 950 955																
CAC His	CAG Gln	GTG Val	GTA Val	CAG Gln	GAC Asp	CTG Leu	CCA Pro	CCT Pro	GCA Ala	AAC Asn	ACA Thr	TTC Phe	GTG Val	GGC Gly	ACC Thr	3410
960 965 970																
GGG Gly	GAC Asp	ACC Thr	ACG Thr	TCC Ser	ACG Thr	GGC Gly	TCT Ser	GAG Glu	CAG Gln	TAC Tyr	TCC Ser	GAC Asp	TAC Tyr	AGC Ser	TAC Tyr	3458
975 980 985																
CGC Arg	ACC Thr	AAC Asn	CCC Pro	CCC Pro	AAA Lys	TAC Tyr	CCC Pro	AGC Ser	AAG Lys	CAG Gln	TTA Leu	CCT Pro	CAC His	CGC Arg	CGC Arg	3506
990 995 1000																
GTC Val	ACC Thr	TTC Phe	TCG Ser	GCC Ala	ACC Thr	AGC Ser	CAG Gln	GCC Ala	CAG Gln	GAG Glu	CTG Leu	CAG Gln	GAC Asp	CCA Pro	TCC Ser	3554
1005 1010 1015 1020																
CAG Gln	CAC His	AGT Ser	TAC Tyr	TAT Tyr	GAC Asp	AGT Ser	GGC Gly	CTG Leu	GAG Glu	GAG Glu	TCT Ser	GAG Glu	ACG Thr	CCG Pro	TCC Ser	3602
1025 1030 1035																
AGC Ser	AAG Lys	TCA Ser	TCC Ser	TCA Ser	GGG Gly	CCT Pro	CGA Arg	CTC Leu	GGT Gly	CCC Pro	CTG Leu	GCC Ala	CTG Leu	CCT Pro	GAG Glu	3650
1040 1045 1050																
GAT Asp	CAC His	TAT Tyr	GAG Glu	CGC Arg	ACC Thr	ACC Thr	CCT Pro	GAT Asp	GGC Gly	AGC Ser	ATA Ile	GGA Gly	GAG Glu	ATG Met	GAG Glu	3698
1055 1060 1065																
CAC His	CCC Pro	GAG Glu	AAT Asn	GAC Asp	CTT Leu	CGC Arg	CCT Pro	TTG Leu	CCT Pro	GAT Asp	GTC Val	GCC Ala	ATG Met	ACA Thr	GGC Gly	3746
1070 1075 1080																
ACA Thr	TGT Cys	ACC Thr	CGG Arg	GAG Glu	TGC Cys	AGT Ser	GAG Glu	TTT Phe	GGC Gly	CAC His	TCT Ser	GAC Asp	ACA Thr	TGC Cys	TGG Trp	3794
1085 1090 1095 1100																
ATG Met	CCT Pro	GGC Gly	CAG Gln	TCA Ser	TCT Ser	CCC Pro	AGC Ser	CGC Arg	CGG Arg	ACC Thr	AAG Lys	AGC Ser	AGC Ser	GCC Ala	CTC Leu	3842
1105 1110 1115																
AAA Lys	CTC Leu	TCC Ser	ACC Thr	TTC Phe	ATG Met	CCT Pro	TAC Tyr	CAG Gln	GAC Asp	CGA Arg	GGA Gly	GGG Gly	CAG Gln	GAG Glu	CCT Pro	3890
1120 1125 1130																
GCG Ala	GGC Gly	GCC Ala	GGC Gly	AGC Ser	CCC Pro	AGC Ser	CCC Pro	CCG Pro	GAA Glu	GAC Asp	CGG Arg	AAC Asn	ACC Thr	AAA Lys	ACG Thr	3938

1135	1140	1145	
GCC CCC GTG CGC CTC CTG CCC TCC TAC AGT GCC TTC TCC CAC AGT AGC			3986
Ala Pro Val Arg Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser			
1150	1155	1160	
CAT GAT TCC TGC AAG GAC TCG GCC ACC TTG GAG GAA ATC CCC CTG ACC			4034
His Asp Ser Cys Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr			
1165	1170	1175	1180
CAG ACC TCG GAC TTC CCA CCC GCA GCC ACA CCG GCA TCT GCC CAG ACG			4082
Gln Thr Ser Asp Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr			
	1185	1190	1195
GCC AAG CGC GAG ATC TAC CTG TGAGCCCCCT ACTGGCCGGC CCCCCTCCCC			4133
Ala Lys Arg Glu Ile Tyr Leu			
1200			
CAGCGCCGGC CAGCTCCCAA ATGCCCATTC CAGGGCCTCA CTCTCCACCC CTTCAGCGTG			4193
GACTTCCTGC CAGGGCCCAA GTGGGGGTAT CACTGACCTC ATGACCACGC TGGCCCTTCT			4253
CCCATGCAGG GTCCAGGTCC TCTCCCCTCA TTTCCATCTC CCAGCCCAGG GGCCCCTTCC			4313
CCTTTATGGG GCTTCCCCCA GCTGATGCCC AAGAGGGCTC CTCTGCAATG ACTGGGCTCC			4373
TTCCCTTGAC TTCCAGGGAG CACCCCCTCG ATTTGGGCAG ATGGTGGAGT CAAGGGTGGG			4433
CAGCGTACTT CTAACTCATT GTTTCCCTCA TGGCCGACCA GGGCGGGGAT AGCATGCCCA			4493
ATTTTAGCCC TGAAGCAGGG CTGAACTGGG GAGCCCCTTT CCCTGGGAGC TCCCAGAGGA			4553
AACTCTTGAC CACCAGTGGC TCCCTGAAGG GCTTTTGTTA CCAAAGGTGG GGTAGGGACG			4613
GGGGTGGGAG TGGAGCGGAG GCCTTGTTTT CCCGTGG			4650

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met	Glu	Pro	Leu	Arg	His	Ser	Pro	Gly	Pro	Gly	Gly	Gln	Arg	Leu	Leu
1					5				10					15	
Leu	Pro	Ser	Met	Leu	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Pro	Ser	Pro	
			20					25					30		
Gly	His	Ala	Thr	Arg	Val	Val	Tyr	Lys	Val	Pro	Glu	Glu	Gln	Pro	Pro
		35					40					45			
Asn	Thr	Leu	Ile	Gly	Ser	Leu	Ala	Ala	Asp	Tyr	Gly	Phe	Pro	Asp	Val
		50				55						60			

Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
65 70 75 80

Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser Ile Asp Arg Glu
85 90 95

Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
100 105 110

Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
115 120 125

Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
130 135 140

Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
145 150 155 160

Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
165 170 175

Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
180 185 190

Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
195 200 205

Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly Ser Pro
210 215 220

Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
225 230 235 240

Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
245 250 255

Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
260 265 270

Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr Phe His Gln Ala
275 280 285

Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg Asn Thr Gly Leu
290 295 300

Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu Ser Thr Leu Arg
305 310 315 320

Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro Lys Ser Ala Arg
325 330 335

Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp Asn Ala Pro Thr
340 345 350

Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln Asp Gly Met Ala
355 360 365

Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val Ala Leu Val Gln
370 375 380

Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val Thr Cys Val Val
385 390 395 400

Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser Glu Thr Gly Ser
405 410 415

Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr Pro Leu Asp Tyr
420 425 430

Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala Val Asp Ser Gly
435 440 445

Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val Gln Val Val Asp
450 455 460

Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val Thr Glu Val Ala
465 470 475 480

Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala Glu Ile Thr Ala
485 490 495

Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val Tyr Ser Leu Glu
500 505 510

Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser Pro Glu Thr Gly
515 520 525

Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln Arg Glu Ser Tyr
530 535 540

Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro Ser Leu Gln Gly
545 550 555 560

Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn Asp Asn Asp Pro
565 570 575

Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met Glu Asn Met Pro
580 585 590

Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp Lys Gly
595 600 605

Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly Asp Phe
610 615 620

Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser Phe Asp
625 630 635 640

Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val Asp Gly
645 650 655

Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn Val Leu
660 665 670

Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn Thr Ser
675 680 685

His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val Ser Gln
690 695 700

Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu Ile Tyr
705 710 715 720

Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly Ser His
725 730 735

Ser	Gly	Ala	Ile	Thr	Leu	Glu	Lys	Glu	Ile	Glu	Arg	Arg	His	His	Gly	
			740					745					750			
Leu	His	Arg	Leu	Val	Val	Lys	Val	Ser	Asp	Arg	Gly	Lys	Pro	Pro	Arg	
		755					760					765				
Tyr	Gly	Thr	Ala	Leu	Val	His	Leu	Tyr	Val	Asn	Glu	Thr	Leu	Ala	Asn	
	770					775					780					
Arg	Thr	Leu	Leu	Glu	Thr	Leu	Leu	Gly	His	Ser	Leu	Asp	Thr	Pro	Leu	
785					790					795					800	
Asp	Ile	Asp	Ile	Ala	Gly	Asp	Pro	Glu	Tyr	Glu	Arg	Ser	Lys	Gln	Arg	
				805					810					815		
Gly	Asn	Ile	Leu	Phe	Gly	Val	Val	Ala	Gly	Val	Val	Ala	Val	Ala	Leu	
		820						825					830			
Leu	Ile	Ala	Leu	Ala	Val	Leu	Val	Arg	Tyr	Cys	Arg	Gln	Arg	Glu	Ala	
		835					840					845				
Lys	Ser	Gly	Tyr	Gln	Ala	Gly	Lys	Lys	Glu	Thr	Lys	Asp	Leu	Tyr	Ala	
	850					855					860					
Pro	Lys	Pro	Ser	Gly	Lys	Ala	Ser	Lys	Gly	Asn	Lys	Ser	Lys	Gly	Lys	
865					870					875					880	
Lys	Ser	Lys	Ser	Pro	Lys	Pro	Val	Lys	Pro	Val	Glu	Asp	Glu	Asp	Glu	
				885					890					895		
Ala	Gly	Leu	Gln	Lys	Ser	Leu	Lys	Phe	Asn	Leu	Met	Ser	Asp	Ala	Pro	
			900					905					910			
Gly	Asp	Ser	Pro	Arg	Ile	His	Leu	Pro	Leu	Asn	Tyr	Pro	Pro	Gly	Ser	
		915					920					925				
Pro	Asp	Leu	Gly	Arg	His	Tyr	Arg	Ser	Asn	Ser	Pro	Leu	Pro	Ser	Ile	
	930					935					940					
Gln	Leu	Gln	Pro	Gln	Ser	Pro	Ser	Ala	Ser	Lys	Lys	His	Gln	Val	Val	
945					950					955					960	
Gln	Asp	Leu	Pro	Pro	Ala	Asn	Thr	Phe	Val	Gly	Thr	Gly	Asp	Thr	Thr	
				965					970					975		
Ser	Thr	Gly	Ser	Glu	Gln	Tyr	Ser	Asp	Tyr	Ser	Tyr	Arg	Thr	Asn	Pro	
			980					985					990			
Pro	Lys	Tyr	Pro	Ser	Lys	Gln	Leu	Pro	His	Arg	Arg	Val	Thr	Phe	Ser	
		995					1000					1005				
Ala	Thr	Ser	Gln	Ala	Gln	Glu	Leu	Gln	Asp	Pro	Ser	Gln	His	Ser	Tyr	
	1010					1015					1020					
Tyr	Asp	Ser	Gly	Leu	Glu	Glu	Ser	Glu	Thr	Pro	Ser	Ser	Lys	Ser	Ser	
1025					1030					1035					1040	
Ser	Gly	Pro	Arg	Leu	Gly	Pro	Leu	Ala	Leu	Pro	Glu	Asp	His	Tyr	Glu	
				1045					1050				1055			
Arg	Thr	Thr	Pro	Asp	Gly	Ser	Ile	Gly	Glu	Met	Glu	His	Pro	Glu	Asn	
			1060					1065					1070			

Asp Leu Arg Pro Leu Pro Asp Val Ala Met Thr Gly Thr Cys Thr Arg
 1075 1080 1085

Glu Cys Ser Glu Phe Gly His Ser Asp Thr Cys Trp Met Pro Gly Gln
 1090 1095 1100

Ser Ser Pro Ser Arg Arg Thr Lys Ser Ser Ala Leu Lys Leu Ser Thr
 1105 1110 1115 1120

Phe Met Pro Tyr Gln Asp Arg Gly Gly Gln Glu Pro Ala Gly Ala Gly
 1125 1130 1135

Ser Pro Ser Pro Pro Glu Asp Arg Asn Thr Lys Thr Ala Pro Val Arg
 1140 1145 1150

Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser His Asp Ser Cys
 1155 1160 1165

Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr Gln Thr Ser Asp
 1170 1175 1180

Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr Ala Lys Arg Glu
 1185 1190 1195 1200

Ile Tyr Leu

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 115..2622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGAAAGCCAT GTCGGACTCG TCGCCAGCG CCAAGCGCT AACCCGCTGA AAGTTTCTCA	60
GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTTGAG TGAG ATG	117
	Met
	1
GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG	165
Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val	
	5 10 15
GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT	213
Gly Val Leu Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile	
	20 25 30
CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC	261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn	
	35 40 45

GTG	GTC	GCG	AAC	CTT	GGT	TTG	GAT	CTC	GGT	AGC	CTC	TCA	GCC	CGC	AGG	309
Val	Val	Ala	Asn	Leu	Gly	Leu	Asp	Leu	Gly	Ser	Leu	Ser	Ala	Arg	Arg	
50					55				60						65	
TTC	CCG	GTG	GTG	TCT	GGA	GCT	AGC	CGA	AGA	TTC	TTT	GAG	GTG	AAC	CGG	357
Phe	Pro	Val	Val	Ser	Gly	Ala	Ser	Arg	Arg	Phe	Phe	Glu	Val	Asn	Arg	
				70					75					80		
GAG	ACC	GGA	GAG	ATG	TTT	GTG	AAC	GAC	CGT	CTG	GAT	CGA	GAG	GAG	CTG	405
Glu	Thr	Gly	Glu	Met	Phe	Val	Asn	Asp	Arg	Leu	Asp	Arg	Glu	Glu	Leu	
			85					90					95			
TGT	GGG	ACA	CTG	CCC	TCT	TGC	ACT	GTA	ACT	CTG	GAG	TTG	GTA	GTG	GAG	453
Cys	Gly	Thr	Leu	Pro	Ser	Cys	Thr	Val	Thr	Leu	Glu	Leu	Val	Val	Glu	
			100				105					110				
AAC	CCG	CTG	GAG	CTG	TTC	AGC	GTG	GAA	GTG	GTG	ATC	CAG	GAC	ATC	AAC	501
Asn	Pro	Leu	Glu	Leu	Phe	Ser	Val	Glu	Val	Val	Ile	Gln	Asp	Ile	Asn	
	115					120					125					
GAC	AAC	AAT	CCT	GCT	TTC	CCT	ACC	CAG	GAA	ATG	AAA	TTG	GAG	ATT	AGC	549
Asp	Asn	Asn	Pro	Ala	Phe	Pro	Thr	Gln	Glu	Met	Lys	Leu	Glu	Ile	Ser	
130					135					140					145	
GAG	GCC	GTG	GCT	CCG	GGG	ACG	CGC	TTT	CCG	CTC	GAG	AGC	GCG	CAC	GAT	597
Glu	Ala	Val	Ala	Pro	Gly	Thr	Arg	Phe	Pro	Leu	Glu	Ser	Ala	His	Asp	
				150					155					160		
CCC	GAT	CTG	GGA	AGC	AAC	TCT	TTA	CAA	ACC	TAT	GAG	CTG	AGC	CGA	AAT	645
Pro	Asp	Leu	Gly	Ser	Asn	Ser	Leu	Gln	Thr	Tyr	Glu	Leu	Ser	Arg	Asn	
			165					170					175			
GAA	TAC	TTT	GCG	CTT	CGC	GTG	CAG	ACG	CGG	GAG	GAC	AGC	ACC	AAG	TAC	693
Glu	Tyr	Phe	Ala	Leu	Arg	Val	Gln	Thr	Arg	Glu	Asp	Ser	Thr	Lys	Tyr	
		180					185					190				
GCG	GAG	CTG	GTG	TTG	GAG	CGC	GCC	CTG	GAC	CGA	GAA	CGG	GAG	CCT	AGT	741
Ala	Glu	Leu	Val	Leu	Glu	Arg	Ala	Leu	Asp	Arg	Glu	Arg	Glu	Pro	Ser	
	195					200					205					
CTC	CAG	TTA	GTG	CTG	ACG	GCG	TTG	GAC	GGA	GGG	ACC	CCA	GCT	CTC	TCC	789
Leu	Gln	Leu	Val	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Thr	Pro	Ala	Leu	Ser	
210					215					220					225	
GCC	AGC	CTG	CCT	ATT	CAC	ATC	AAG	GTG	CTG	GAC	GCG	AAT	GAC	AAT	GCG	837
Ala	Ser	Leu	Pro	Ile	His	Ile	Lys	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	
			230						235					240		
CCT	GTC	TTC	AAC	CAG	TCC	TTG	TAC	CGG	GCG	CGC	GTT	CCT	GGA	GGA	TGC	885
Pro	Val	Phe	Asn	Gln	Ser	Leu	Tyr	Arg	Ala	Arg	Val	Pro	Gly	Gly	Cys	
			245					250					255			
ACC	TCC	GGC	ACG	CGC	GTG	GTA	CAA	GTC	CTT	GCA	ACG	GAT	CTG	GAT	GAA	933
Thr	Ser	Gly	Thr	Arg	Val	Val	Gln	Val	Leu	Ala	Thr	Asp	Leu	Asp	Glu	
		260					265					270				
GGC	CCC	AAC	GGT	GAA	ATT	ATT	TAC	TCC	TTC	GGC	AGC	CAC	AAC	CGC	GCC	981
Gly	Pro	Asn	Gly	Glu	Ile	Ile	Tyr	Ser	Phe	Gly	Ser	His	Asn	Arg	Ala	
	275					280					285					

GGC	GTG	CGG	CAA	CTA	TTC	GCC	TTA	GAC	CTT	GTA	ACC	GGG	ATG	CTG	ACA	1029
Gly	Val	Arg	Gln	Leu	Phe	Ala	Leu	Asp	Leu	Val	Thr	Gly	Met	Leu	Thr	
290					295					300					305	
ATC	AAG	GGT	CGG	CTG	GAC	TTC	GAG	GAC	ACC	AAA	CTC	CAT	GAG	ATT	TAC	1077
Ile	Lys	Gly	Arg	Leu	Asp	Phe	Glu	Asp	Thr	Lys	Leu	His	Glu	Ile	Tyr	
				310					315					320		
ATC	CAG	GCC	AAA	GAC	AAG	GGC	GCC	AAT	CCC	GAA	GGA	GCA	CAT	TGC	AAA	1125
Ile	Gln	Ala	Lys	Asp	Lys	Gly	Ala	Asn	Pro	Glu	Gly	Ala	His	Cys	Lys	
			325					330					335			
GTG	TTG	GTG	GAG	GTT	GTG	GAT	GTG	AAT	GAC	AAC	GCC	CCG	GAG	ATC	ACA	1173
Val	Leu	Val	Glu	Val	Val	Asp	Val	Asn	Asp	Asn	Ala	Pro	Glu	Ile	Thr	
		340					345					350				
GTC	ACC	TCC	GTG	TAC	AGC	CCA	GTA	CCC	GAG	GAT	GCC	TCT	GGG	ACT	GTC	1221
Val	Thr	Ser	Val	Tyr	Ser	Pro	Val	Pro	Glu	Asp	Ala	Ser	Gly	Thr	Val	
	355					360					365					
ATC	GCT	TTG	CTC	AGT	GTG	ACT	GAC	CTG	GAT	GCT	GGC	GAG	AAC	GGG	CTG	1269
Ile	Ala	Leu	Leu	Ser	Val	Thr	Asp	Leu	Asp	Ala	Gly	Glu	Asn	Gly	Leu	
370					375					380					385	
GTG	ACC	TGC	GAA	GTT	CCA	CCG	GGT	CTC	CCT	TTC	AGC	CTT	ACT	TCT	TCC	1317
Val	Thr	Cys	Glu	Val	Pro	Pro	Gly	Leu	Pro	Phe	Ser	Leu	Thr	Ser	Ser	
				390					395					400		
CTC	AAG	AAT	TAC	TTC	ACT	TTG	AAA	ACC	AGT	GCA	GAC	CTG	GAT	CGG	GAG	1365
Leu	Lys	Asn	Tyr	Phe	Thr	Leu	Lys	Thr	Ser	Ala	Asp	Leu	Asp	Arg	Glu	
			405					410					415			
ACT	GTG	CCA	GAA	TAC	AAC	CTC	AGC	ATC	ACC	GCC	CGA	GAC	GCC	GGA	ACC	1413
Thr	Val	Pro	Glu	Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Gly	Thr	
		420					425					430				
CCT	TCC	CTC	TCA	GCC	CTT	ACA	ATA	GTG	CGT	GTT	CAA	GTG	TCC	GAC	ATC	1461
Pro	Ser	Leu	Ser	Ala	Leu	Thr	Ile	Val	Arg	Val	Gln	Val	Ser	Asp	Ile	
	435					440					445					
AAT	GAC	AAC	CCT	CCA	CAA	TCT	TCT	CAA	TCT	TCC	TAC	GAC	GTT	TAC	ATT	1509
Asn	Asp	Asn	Pro	Pro	Gln	Ser	Ser	Gln	Ser	Ser	Tyr	Asp	Val	Tyr	Ile	
450					455					460					465	
GAA	GAA	AAC	AAC	CTC	CCC	GGG	GCT	CCA	ATA	CTA	AAC	CTA	AGT	GTC	TGG	1557
Glu	Glu	Asn	Asn	Leu	Pro	Gly	Ala	Pro	Ile	Leu	Asn	Leu	Ser	Val	Trp	
				470				475						480		
GAC	CCC	GAC	GCC	CCG	CAG	AAT	GCT	CGG	CTT	TCT	TTC	TTT	CTC	TTG	GAG	1605
Asp	Pro	Asp	Ala	Pro	Gln	Asn	Ala	Arg	Leu	Ser	Phe	Phe	Leu	Leu	Glu	
			485					490					495			
CAA	GGA	GCT	GAA	ACC	GGG	CTA	GTG	GGT	CGC	TAT	TTC	ACA	ATA	AAT	CGT	1653
Gln	Gly	Ala	Glu	Thr	Gly	Leu	Val	Gly	Arg	Tyr	Phe	Thr	Ile	Asn	Arg	
		500					505					510				
GAC	AAT	GGC	ATA	GTG	TCA	TCC	TTA	GTG	CCC	CTA	GAC	TAT	GAG	GAT	CGG	1701
Asp	Asn	Gly	Ile	Val	Ser	Ser	Leu	Val	Pro	Leu	Asp	Tyr	Glu	Asp	Arg	
	515					520					525					

CGG Arg 530	GAA Glu	TTT Phe	GAA Glu	TTA Leu	ACA Thr	GCT Ala	CAT His	ATC Ile	AGC Ser	GAT Asp	GGG Gly	GGC Gly	ACC Thr	CCG Pro	GTC Val	1749
CTA Leu	GCC Ala	ACC Thr	AAC Asn	ATC Ile	AGC Ser	GTG Val	AAC Asn	ATA Ile	TTT Phe	GTC Val	ACT Thr	GAT Asp	CGC Arg	AAT Asn	GAC Asp	1797
AAT Asn	GCC Ala	CCC Pro	CAG Gln	GTC Val	CTA Leu	TAT Tyr	CCT Pro	CGG Arg	CCA Pro	GGT Gly	GGG Gly	AGC Ser	TCG Ser	GTG Val	GAG Glu	1845
ATG Met	CTG Leu	CCT Pro	CGA Arg	GGT Gly	ACC Thr	TCA Ser	GCT Ala	GGC Gly	CAC His	CTA Leu	GTG Val	TCA Ser	CGG Arg	GTG Val	GTA Val	1893
GGC Gly	TGG Trp	GAC Asp	GCG Ala	GAT Asp	GCA Ala	GGG Gly	CAC His	AAT Asn	GCC Ala	TGG Trp	CTC Leu	TCC Ser	TAC Tyr	AGT Ser	CTC Leu	1941
TTT Phe 610	GGA Gly	TCC Ser	CCT Pro	AAC Asn	CAG Gln	AGC Ser	CTT Leu	TTT Phe	GCC Ala	ATA Ile	GGG Gly	CTG Leu	CAC His	ACT Thr	GGT Gly	1989
CAA Gln	ATC Ile	AGT Ser	ACT Thr	GCC Ala	CGT Arg	CCA Pro	GTC Val	CAA Gln	GAC Asp	ACA Thr	GAT Asp	TCA Ser	CCC Pro	AGG Arg	CAG Gln	2037
ACT Thr	CTC Leu	ACT Thr	GTC Val	TTG Leu	ATC Ile	AAA Lys	GAC Asp	AAT Asn	GGG Gly	GAG Glu	CCT Pro	TCG Ser	CTC Leu	TCC Ser	ACC Thr	2085
ACT Thr	GCT Ala	ACC Thr	CTC Leu	ACT Thr	GTG Val	TCA Ser	GTA Val	ACC Thr	GAG Glu	GAC Asp	TCT Ser	CCT Pro	GAA Glu	GCC Ala	CGA Arg	2133
GCC Ala	GAG Glu	TTC Phe	CCC Pro	TCT Ser	GGC Gly	TCT Ser	GCC Ala	CCC Pro	CGG Arg	GAG Glu	CAG Gln	AAA Lys	AAA Lys	AAT Asn	CTC Leu	2181
ACC Thr	TTT Phe	TAT Tyr	CTA Leu	CTT Leu	CTT Leu	TCT Ser	CTA Leu	ATC Ile	CTG Leu	GTT Val	TCT Ser	GTG Val	GGC Gly	TTC Phe	GTG Val	2229
GTC Val	ACA Thr	GTG Val	TTC Phe	GGA Gly	GTA Val	ATC Ile	ATA Ile	TTC Phe	AAA Lys	GTT Val	TAC Tyr	AAG Lys	TGG Trp	AAG Lys	CAG Gln	2277
TCT Ser	AGA Arg	GAC Asp	CTA Leu	TAC Tyr	CGA Arg	GCC Ala	CCG Pro	GTG Val	AGC Ser	TCA Ser	CTG Leu	TAC Tyr	CGA Arg	ACA Thr	CCA Pro	2325
GGG Gly	CCC Pro	TCC Ser	TTG Leu	CAC His	GCG Ala	GAC Asp	GCC Ala	GTG Val	CGG Arg	GGA Gly	GGC Gly	CTG Leu	ATG Met	TCG Ser	CCG Pro	2373
CAC His	CTT Leu	TAC Tyr	CAT His	CAG Gln	GTG Val	TAT Tyr	CTC Leu	ACC Thr	ACG Thr	GAC Asp	TCC Ser	CGC Arg	CGC Arg	AGC Ser	GAC Asp	2421

CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG	2469
Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln	
770 775 780 785	
AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT	2517
Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly	
790 795 800	
GCA GAG AGC GCC CCT CCC GGA CAG GTA AGG TTT AGC AAG TCA TGC TTG	2565
Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys Leu	
805 810 815	
ACC CTG TTA GTG CCT TTT TAT TCC TAC ATC ATA TTG AGA AGG CTG GAG	2613
Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu Glu	
820 825 830	
CTG TTT TTT TAGTGATGAA GATGTTTTCC TGGTGATGCA TTCACACTTT	2662
Leu Phe Phe	
835	
CAACTGGCTC TTCCTAGATC AAAGTTAGTG CCTTTGTGAG ATGGTGGCCT GCCAGAGTGT	2722
GGTTTGTGGT CCCATTTTCAG GGGGAAGATA CTTGACTCAT CTGTGGACCT AATTCACATC	2782
CTCAGCG	2789

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val	
1 5 10 15	
Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val	
20 25 30	
Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly	
35 40 45	
Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg	
50 55 60	
Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn	
65 70 75 80	
Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu	
85 90 95	
Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val	
100 105 110	
Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile	
115 120 125	

Asn	Asp	Asn	Asn	Pro	Ala	Phe	Pro	Thr	Gln	Glu	Met	Lys	Leu	Glu	Ile	130	135	140
Ser	Glu	Ala	Val	Ala	Pro	Gly	Thr	Arg	Phe	Pro	Leu	Glu	Ser	Ala	His	145	150	155
Asp	Pro	Asp	Leu	Gly	Ser	Asn	Ser	Leu	Gln	Thr	Tyr	Glu	Leu	Ser	Arg	165	170	175
Asn	Glu	Tyr	Phe	Ala	Leu	Arg	Val	Gln	Thr	Arg	Glu	Asp	Ser	Thr	Lys	180	185	190
Tyr	Ala	Glu	Leu	Val	Leu	Glu	Arg	Ala	Leu	Asp	Arg	Glu	Arg	Glu	Pro	195	200	205
Ser	Leu	Gln	Leu	Val	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Thr	Pro	Ala	Leu	210	215	220
Ser	Ala	Ser	Leu	Pro	Ile	His	Ile	Lys	Val	Leu	Asp	Ala	Asn	Asp	Asn	225	230	235
Ala	Pro	Val	Phe	Asn	Gln	Ser	Leu	Tyr	Arg	Ala	Arg	Val	Pro	Gly	Gly	245	250	255
Cys	Thr	Ser	Gly	Thr	Arg	Val	Val	Gln	Val	Leu	Ala	Thr	Asp	Leu	Asp	260	265	270
Glu	Gly	Pro	Asn	Gly	Glu	Ile	Ile	Tyr	Ser	Phe	Gly	Ser	His	Asn	Arg	275	280	285
Ala	Gly	Val	Arg	Gln	Leu	Phe	Ala	Leu	Asp	Leu	Val	Thr	Gly	Met	Leu	290	295	300
Thr	Ile	Lys	Gly	Arg	Leu	Asp	Phe	Glu	Asp	Thr	Lys	Leu	His	Glu	Ile	305	310	315
Tyr	Ile	Gln	Ala	Lys	Asp	Lys	Gly	Ala	Asn	Pro	Glu	Gly	Ala	His	Cys	325	330	335
Lys	Val	Leu	Val	Glu	Val	Val	Asp	Val	Asn	Asp	Asn	Ala	Pro	Glu	Ile	340	345	350
Thr	Val	Thr	Ser	Val	Tyr	Ser	Pro	Val	Pro	Glu	Asp	Ala	Ser	Gly	Thr	355	360	365
Val	Ile	Ala	Leu	Leu	Ser	Val	Thr	Asp	Leu	Asp	Ala	Gly	Glu	Asn	Gly	370	375	380
Leu	Val	Thr	Cys	Glu	Val	Pro	Pro	Gly	Leu	Pro	Phe	Ser	Leu	Thr	Ser	385	390	395
Ser	Leu	Lys	Asn	Tyr	Phe	Thr	Leu	Lys	Thr	Ser	Ala	Asp	Leu	Asp	Arg	405	410	415
Glu	Thr	Val	Pro	Glu	Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Gly	420	425	430
Thr	Pro	Ser	Leu	Ser	Ala	Leu	Thr	Ile	Val	Arg	Val	Gln	Val	Ser	Asp	435	440	445
Ile	Asn	Asp	Asn	Pro	Pro	Gln	Ser	Ser	Gln	Ser	Ser	Tyr	Asp	Val	Tyr	450	455	460

Ile	Glu	Glu	Asn	Asn	Leu	Pro	Gly	Ala	Pro	Ile	Leu	Asn	Leu	Ser	Val	465	470	475				480
Trp	Asp	Pro	Asp	Ala	Pro	Gln	Asn	Ala	Arg	Leu	Ser	Phe	Phe	Leu	Leu		485	490				495
Glu	Gln	Gly	Ala	Glu	Thr	Gly	Leu	Val	Gly	Arg	Tyr	Phe	Thr	Ile	Asn		500	505				510
Arg	Asp	Asn	Gly	Ile	Val	Ser	Ser	Leu	Val	Pro	Leu	Asp	Tyr	Glu	Asp		515	520				525
Arg	Arg	Glu	Phe	Glu	Leu	Thr	Ala	His	Ile	Ser	Asp	Gly	Gly	Thr	Pro		530	535				540
Val	Leu	Ala	Thr	Asn	Ile	Ser	Val	Asn	Ile	Phe	Val	Thr	Asp	Arg	Asn		545	550				555
Asp	Asn	Ala	Pro	Gln	Val	Leu	Tyr	Pro	Arg	Pro	Gly	Gly	Ser	Ser	Val		565	570				575
Glu	Met	Leu	Pro	Arg	Gly	Thr	Ser	Ala	Gly	His	Leu	Val	Ser	Arg	Val		580	585				590
Val	Gly	Trp	Asp	Ala	Asp	Ala	Gly	His	Asn	Ala	Trp	Leu	Ser	Tyr	Ser		595	600				605
Leu	Phe	Gly	Ser	Pro	Asn	Gln	Ser	Leu	Phe	Ala	Ile	Gly	Leu	His	Thr		610	615				620
Gly	Gln	Ile	Ser	Thr	Ala	Arg	Pro	Val	Gln	Asp	Thr	Asp	Ser	Pro	Arg		625	630				635
Gln	Thr	Leu	Thr	Val	Leu	Ile	Lys	Asp	Asn	Gly	Glu	Pro	Ser	Leu	Ser		645	650				655
Thr	Thr	Ala	Thr	Leu	Thr	Val	Ser	Val	Thr	Glu	Asp	Ser	Pro	Glu	Ala		660	665				670
Arg	Ala	Glu	Phe	Pro	Ser	Gly	Ser	Ala	Pro	Arg	Glu	Gln	Lys	Lys	Asn		675	680				685
Leu	Thr	Phe	Tyr	Leu	Leu	Leu	Ser	Leu	Ile	Leu	Val	Ser	Val	Gly	Phe		690	695				700
Val	Val	Thr	Val	Phe	Gly	Val	Ile	Ile	Phe	Lys	Val	Tyr	Lys	Trp	Lys		705	710				715
Gln	Ser	Arg	Asp	Leu	Tyr	Arg	Ala	Pro	Val	Ser	Ser	Leu	Tyr	Arg	Thr		725	730				735
Pro	Gly	Pro	Ser	Leu	His	Ala	Asp	Ala	Val	Arg	Gly	Gly	Leu	Met	Ser		740	745				750
Pro	His	Leu	Tyr	His	Gln	Val	Tyr	Leu	Thr	Thr	Asp	Ser	Arg	Arg	Ser		755	760				765
Asp	Pro	Leu	Leu	Lys	Lys	Pro	Gly	Ala	Ala	Ser	Pro	Leu	Ala	Ser	Arg		770	775				780
Gln	Asn	Thr	Leu	Arg	Ser	Cys	Asp	Pro	Val	Phe	Tyr	Arg	Gln	Val	Leu		785	790				795

Gly Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys
805 810 815
Leu Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu
820 825 830
Glu Leu Phe Phe
835

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 115..2160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CGAAAGCCAT GTCGGACTCG TCGCCAGCG CCAAGCGCT AACCCGCTGA AAGTTTCTCA	60
GCGAAATCTC AGGGACGATC TGGACCCGC TGAGAGGAAC TGCTTTTGAG TGAG ATG	117
Met	
1	
GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG	165
Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val	
5 10 15	
GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT	213
Gly Val Leu Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile	
20 25 30	
CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC	261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn	
35 40 45	
GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG	309
Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg	
50 55 60 65	
TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG	357
Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg	
70 75 80	
GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG	405
Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu	
85 90 95	
TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG	453
Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu	
100 105 110	

AAC Asn 115	CCG Pro	CTG Leu	GAG Glu	CTG Leu	TTC Phe	AGC Ser	GTG Val	GAA Glu	GTG Val	GTG Val	ATC Ile	CAG Gln	GAC Asp	ATC Ile	AAC Asn	501
GAC Asp 130	AAC Asn	AAT Asn	CCT Pro	GCT Ala	TTC Phe	CCT Pro	ACC Thr	CAG Gln	GAA Glu	ATG Met	AAA Lys	TTG Leu	GAG Glu	ATT Ile	AGC Ser	549
GAG Glu	GCC Ala	GTG Val	GCT Ala	CCG Pro	GGG Gly	ACG Thr	CGC Arg	TTT Phe	CCG Pro	CTC Leu	GAG Glu	AGC Ser	GCG Ala	CAC His	GAT Asp	597
CCC Pro	GAT Asp	CTG Leu	GGA Gly	AGC Ser	AAC Asn	TCT Ser	TTA Leu	CAA Gln	ACC Thr	TAT Tyr	GAG Glu	CTG Leu	AGC Ser	CGA Arg	AAT Asn	645
GAA Glu	TAC Tyr	TTT Phe	GCG Ala	CTT Leu	CGC Arg	GTG Val	CAG Gln	ACG Thr	CGG Arg	GAG Glu	GAC Asp	AGC Ser	ACC Thr	AAG Lys	TAC Tyr	693
GCG Ala	GAG Glu	CTG Leu	GTG Val	TTG Leu	GAG Glu	CGC Arg	GCC Ala	CTG Leu	GAC Asp	CGA Arg	GAA Glu	CGG Arg	GAG Glu	CCT Pro	AGT Ser	741
CTC Leu	CAG Gln	TTA Leu	GTG Val	CTG Leu	ACG Thr	GCG Ala	TTG Leu	GAC Asp	GGA Gly	GGG Gly	ACC Thr	CCA Pro	GCT Ala	CTC Leu	TCC Ser	789
GCC Ala	AGC Ser	CTG Leu	CCT Pro	ATT Ile	CAC His	ATC Ile	AAG Lys	GTG Val	CTG Leu	GAC Asp	GCG Ala	AAT Asn	GAC Asp	AAT Asn	GCG Ala	837
CCT Pro	GTC Val	TTC Phe	AAC Asn	CAG Gln	TCC Ser	TTG Leu	TAC Tyr	CGG Arg	GCG Ala	CGC Arg	GTT Val	CCT Pro	GGA Gly	GGA Gly	TGC Cys	885
ACC Thr	TCC Ser	GGC Gly	ACG Thr	CGC Arg	GTG Val	GTA Val	CAA Gln	GTC Val	CTT Leu	GCA Ala	ACG Thr	GAT Asp	CTG Leu	GAT Asp	GAA Glu	933
GGC Gly	CCC Pro	AAC Asn	GGT Gly	GAA Glu	ATT Ile	ATT Ile	TAC Tyr	TCC Ser	TTC Phe	GGC Gly	AGC Ser	CAC His	AAC Asn	CGC Arg	GCC Ala	981
GGC Gly	GTG Val	CGG Arg	CAA Gln	CTA Leu	TTC Phe	GCC Ala	TTA Leu	GAC Asp	CTT Leu	GTA Val	ACC Thr	GGG Gly	ATG Met	CTG Leu	ACA Thr	1029
ATC Ile	AAG Lys	GGT Gly	CGG Arg	CTG Leu	GAC Asp	TTC Phe	GAG Glu	GAC Asp	ACC Thr	AAA Lys	CTC Leu	CAT His	GAG Glu	ATT Ile	TAC Tyr	1077
ATC Ile	CAG Gln	GCC Ala	AAA Lys	GAC Asp	AAG Lys	GGC Gly	GCC Ala	AAT Asn	CCC Pro	GAA Glu	GGA Gly	GCA Ala	CAT His	TGC Cys	AAA Lys	1125
GTG Val	TTG Leu	GTG Val	GAG Glu	GTT Val	GTG Val	GAT Asp	GTG Val	AAT Asn	GAC Asp	AAC Asn	GCC Ala	CCG Pro	GAG Glu	ATC Ile	ACA Thr	1173

GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC	1221
Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val	
355 360 365	
ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG	1269
Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu	
370 375 380 385	
GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC	1317
Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser	
390 395 400	
CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG	1365
Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu	
405 410 415	
ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC	1413
Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr	
420 425 430	
CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC	1461
Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile	
435 440 445	
AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT	1509
Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr Ile	
450 455 460 465	
GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA CTA AAC CTA AGT GTC TGG	1557
Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp	
470 475 480	
GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG	1605
Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu Glu	
485 490 495	
CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT	1653
Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg	
500 505 510	
GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG	1701
Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg	
515 520 525	
CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGC GGC ACC CCG GTC	1749
Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val	
530 535 540 545	
CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC	1797
Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp	
550 555 560	
AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG	1845
Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu	
565 570 575	
ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA	1893
Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val	
580 585 590	

GGC TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC	1941
Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu	
595 600 605	
TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT	1989
Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly	
610 615 620 625	
CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG	2037
Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln	
630 635 640	
ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC	2085
Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr	
645 650 655	
ACT GCT ACC CTC ACT GTG TCA GTA ACC GAG GAC TCT CCT GAA GCC CGA	2133
Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg	
660 665 670	
GCC GAG TTC CCC TCT GGC TCT GCC AGT TAAACCTTCT TTAATTATGG	2180
Ala Glu Phe Pro Ser Gly Ser Ala Ser	
675 680	
ATTAGCCATT AACATTTTTG AAACGTGGAC CATTTAACCT CGGCCTACCC CCTCCAAC TG	2240
TCCTGGTGAT GAGTTCATTA GCTAAGTTAA ATTAATTGAA CTTTGATCTA AACC AAAACA	2300
AATCAGGAAA ATAAAGCTGT AAAGGAACTT ATCAAGCATT CCAA AACCAA CTAGAAATTA	2360
CTTGAAGTTT CGAGTGAGCA TTGCCTGTGC CAGTATTCTT CATTATAGGA TTATAAACTC	2420
GTTTTTTTCC CAAAGCGCAT GTCTACGCCA GGCAGAGGAG TAATTATTCA GCCAATTTCA	2480
TGGATGTAAC GATGGATATA AATAATTGAT AGCACCTAGA GGCTTCCAGT TTGGGTGGAA	2540
GGCTAAAAGT AGAGGGGAAC TCACTCACTT GAGAAATGAT ATTTAAGTGA ATAAATAGTT	2600
CTCTTCTATG AAAC TATTAC TATTTAGTTC TCTGGAAAAC TTAAGTGTAT TAATGATTAG	2660
AACATCAAAT CCTAAGTAAA GAAATGACAT TTAAATATA AAAAGCCAAA CTTTAAATAA	2720
ATCATAGAGA CCTCAGACAT AATATAGGAA A	2751

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val
1 5 10 15
Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val
20 25 30

Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly
35 40 45

Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg
50 55 60

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
65 70 75 80

Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
85 90 95

Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
100 105 110

Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
260 265 270

Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
275 280 285

Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
290 295 300

Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
305 310 315 320

Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
325 330 335

Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
340 345 350

Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
355 360 365

Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
370 375 380

Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
385 390 395 400

Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
405 410 415

Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
420 425 430

Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
435 440 445

Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
450 455 460

Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
465 470 475 480

Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
485 490 495

Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
500 505 510

Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
515 520 525

Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
530 535 540

Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
545 550 555 560

Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
565 570 575

Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
580 585 590

Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
595 600 605

Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
610 615 620

Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
625 630 635 640

Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
645 650 655

Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
660 665 670

Arg Ala Glu Phe Pro Ser Gly Ser Ala Ser
675 680

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCA CGAGGCTGAA CTGAGGGTGA CGGACATAAA CGACTATTCT CCAGTGTTCA	60
GTGAAAGAGA AATGATACTG AGGATACCAG AAAACAGTGC TCGGGGAAAT ACATTCCCTT	120
TAAACAATGC TCTGGACTCA GACGTAGATA TCAACAATAT CCAGACCTAT AGGCTCAGCT	180
CAAACCTCTCA TTTCCTGGTT GTAACCCGCA ACCGCAGTGA TGGCAGGAAG TACCCAGAGC	240
TGGTGCTGGA GAAAGAACTG GATCGAGAGG AGGAACCTGA GCTGAGGTTA ACGCTGACAG	300
CTTTGGATGG TGGCTCTCCT CCCCGGTCTG GGACGACACA GGTCTTCATT GAAGTAGTGG	360
ACACCAACGA TAATGCACCC GAGTTTCAGC AGCCAACATA CCAAGTGCAA ACTCCCGAGA	420
ACAGTCCCAC CGGCTCTCTG GTACTCACAG TCTCAGCCAA TGACTTAGAC AGTGGAGACT	480
ATGGGAAAGT CTTGTACGCA CTTTCGCAAC CCTCAGAAGA TATTAGCAAA ACATTCGAGG	540
TAAACCCCTGT AACCAGGGGAA ATTTCGCCTAC GAAAAGAGGT GAATTTTGAA ACTATTCCTT	600
CGTATGAAGT GGTTATCAAG GGGACGGACG GGGGAGGTCT CTCAGGAAAA TGCACTCTGT	660
TACTGCAGGT GGTGGACGTG AATGACAATG CCCAGAAGT GATGCTATCT GCGCTAACCA	720
ACCCAGTCCC AGAAAATTCC CCCGATGAGG TAGTGGCTGT TTTCAGTGTT AGAGATCCTG	780
ACTCTGGGAA CAACGGAAAA GTGATTGCAT CCATCGAGGA AGACCTGCCC TTTCTTCTAA	840
AATCTTCAGG AAAGAACTTT TACACTTTAG TAACCAAGGG AGCACTTGAC AGGGAAGAAA	900
GAGAGCAATT GAACATCACC ATCACAGTCA CTGACCTGGG CATACCCAGG CTCACCACCC	960
AACACACCAT AACAGTGCAG GTGGCAGACA TCAACGACAA TGCCCCCTCC TTCACCCAAA	1020
CCTCCTACAC CATGTTTGTC CGCGAGAACA ACAGCCCCGC CCTGCACATA GGCACCATCA	1080
GCGCCACAGA CTCAGACTCA GGATCCAATG CCCACATCAC CTACTCGCTG CTACCGCCCC	1140
AAGACCCACA GCTGGCCCTC GACTCGCTCA TCTCCATCAA TGTAGACAAC GGGCAGCTGT	1200
TCGCGCTCAG GCGCTAGAC TATGAGGCTC TGCAGGGCTT CGAGTTCCAT GTGGGCGCCA	1260
CAGACCAAGG CTCGCCC GCG CTCAGCAGCC AGGCTCTGGT GCACGTGGTG GTGTTGGACG	1320
ACAATGACAA TGCGCCCTTC GTGCTCTACC CGCTGCAAAA CGCCTCTGCA CCCTTCACTG	1380
AGCTGCTGCC CAGGGCGGCA GAGCCTGGAT ACCTGGTTAC CAAGGTGGTA GCTGTGGACC	1440
GCGACTCTGG CCAGAATGCC TGGCTGTCAT TCCAGCTGCT CAAGGCCACG GAGCCCGGGC	1500

TGTTCAACGT ATGGGCGCAC AATGGCGAGG TACGCACCTC CAGGCTGCTG AGCGAGCGCG	1560
ACGCACCCAA GCACAAGCTG CTGCTGTTGG TCAAGGACAA TGGAGATCCT CCACGCTCTG	1620
CCAGTGTAC TCTGCACGTG CTAGTGGTGG ATGCCCTTCTC TCAGCCCTAC CTGCCTCTGC	1680
CAGAGGTGGC GCACGACCCT GCACAAGAAG AAGATGCGCT AACACTCTAC CTGGTCATAG	1740
CTTTGGCATC TGTGTCTTCT CTCTTCCTCT TGTCTGTGCT GCTGTTTCGTG GGGGTGAGGC	1800
TCTGCAGGAG GGCCAGGGCA GCCTCTCTGA GTGCCATTTC TGTGCCTGAA GGCCACTTTC	1860
CTGGCCAGCT GGTGGATGTC AGAGGTATGG GGACCCTGTC CCAGAGCTAC CAGTATGATG	1920
TATGTCTGAT GGGGGATTCT TCTGGGACCA GCGAATTTAA CTTCTTAAAG CCAGTCTGTC	1980
CTAGCTCTCT GCACCAAGTGC TCTGGGAAAG AAATAGAGGA AAATTCCACA CTCCAGAATA	2040
GTTTTGGGTT TCATCATTA TAGAAAACTA CTTTACAGAT ATTTAATTCC AAATATCATC	2100
TTGTTGATTA ACTAAAGTCT GTTCACATGT AGCTAGCTAG CAACGATTTT AATGTTCACT	2160
TTACCCATCT TTTTTCAGGG TCATGTCTAA AGCTACAAGT TTGNCTTTAC TTATACTTGT	2220
CGCACAGAAT NNNNNNNNNN TGGTGTATAA GTCACAGTCA TGGGATACTG GCACAAGATG	2280
GCAGCTTGAT TGCTCAGTTA TGGCTGCAAA GGGGNGCTTG AGTTTAGGGA ATGTGTTAGA	2340
GCTGGAATAA GTTTTCTGAG AAATGTGTAA GACAAATTTT TTTTGCACAT TCCCTGTGTT	2400
CCTGTACCCC TGTTTCCAGA ACTACGAAAT GTGTCATCAG AAGGCATGCT CACATTTTCC	2460
CCTTTGTTTG CGTGACCCGG GTGCCAGAAA TTAAATAAAA TTAGCATGGA GTTCAATGCA	2520
GCATTAAAAC AAAGTTACTT CTACAAACCT TTTATTCGAC GGTAAAAATT GTAACCTCCC	2580
CACCCATGAG GCTGGCTGTA AGAACCAGTA TGAATGGGTG TCTATCGCAA CCTTATTTTC	2640
AAAAATCAAA CAAAAGGAGA AATGAGAGAC CAAACAACAC GCTACAGGAA AGATTTTATA	2700
AGGATGTATG TATGGACACA AAAACTGGGA TACAGACATT TTAAATCTGT TGGTACCACA	2760
TGGTGGCGCT GCAGGCTAAA GAAATGCAAG GGAAATTTAA AAGAGGCTGA GCTAGAAGTC	2820
AAAAAAAAA A	2831

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 763..3123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTATTTTTC	ACAGTTTAA	ATTTTCATA	AATCATAACT	CTCTGACTTT	ATGTAGAAAG	60
GATACCACAC	TGGAATTAAC	GTGTAGCTTT	TTCTTGATGT	AATCCAACCA	ATGGGAGCAC	120
AATTCTGGTA	CATAGGCTGT	CTAGAATTTG	AAAGAAATTA	AAGAATTCAT	TTTGTTTTGC	180
TGATAAATTT	TTAAGAAATC	ACGTGGCTTT	ATGTTATTAT	TATTACAAGA	TGACTGATCA	240
CTATTATGTC	TTCTTTTCACT	TCTCAATTTT	CCTCAGAACA	CTACACCCAG	ACTACAGGCT	300
CTGGAGGGTG	GGGACCATGT	CTGGGTTGTT	TACTGATGTA	TTTCATAATT	TGGCACATAG	360
AGACCAATAA	TACTCCTTTA	AATGAAGAAA	TTAATAATTA	CCATTGCGTG	ATATTGTGAT	420
TACATCATTT	CCTCCCAATT	TCCAAACTCC	TAATAGAATA	GAGAATAGAT	CAATTGTAGC	480
AATTCGTTTC	GAAGCAAAGA	CAACGCATGG	TGGCGCTGCA	GGCTAAGGCT	TCAAAAAAAG	540
GAAAAGGAAA	AAGCCCATGA	AATGCTACTA	GCTACTTCAG	ACCTCTTTCA	GCCTAAGAGG	600
AAAGCCTGTT	AGCAGAGCAC	GGACCAGTGT	CTCCGGAGAA	TGCTATTCTC	CTACATTTCC	660
GAACAGGTTA	TCAACGCACA	GATCGATCAC	TGCCTCTGTC	CCATCGCTCC	CTGAAGTAGC	720
TCTGACTCCG	GTTCTTGAA	AGGGGCGTGT	ACAGAAGTAA	AG ATG GAG CCT GCA	Met Glu Pro Ala	774
				1		
GGG GAG CGC TTT CCC GAA CAA AGG CAA GTC CTG ATT CTC CTT CTT TTA	822					
Gly Glu Arg Phe Pro Glu Gln Arg Gln Val Leu Ile Leu Leu Leu Leu						
5 10 15 20						
CTG GAA GTG ACT CTG GCA GGC TGG GAA CCC CGT CGC TAT TCT GTG ATG	870					
Leu Glu Val Thr Leu Ala Gly Trp Glu Pro Arg Arg Tyr Ser Val Met						
25 30 35						
GAG GAA ACA GAG AGA GGT TCT TTT GTA GCC AAC CTG GCC AAT GAC CTA	918					
Glu Glu Thr Glu Arg Gly Ser Phe Val Ala Asn Leu Ala Asn Asp Leu						
40 45 50						
GGG CTG GGA GTG GGG GAG CTA GCC GAG CGG GGA GCC CGG GTA GTT TCT	966					
Gly Leu Gly Val Gly Glu Leu Ala Glu Arg Gly Ala Arg Val Val Ser						
55 60 65						
GAG GAT AAC GAA CAA GGC TTG CAG CTT GAT CTG CAG ACC GGG CAG TTG	1014					
Glu Asp Asn Glu Gln Gly Leu Gln Leu Asp Leu Gln Thr Gly Gln Leu						
70 75 80						
ATA TTA AAT GAG AAG CTG GAC CGG GAG AAG CTG TGT GGC CCT ACT GAG	1062					
Ile Leu Asn Glu Lys Leu Asp Arg Glu Lys Leu Cys Gly Pro Thr Glu						
85 90 95 100						
CCC TGT ATA ATG CAT TTC CAA GTG TTA CTG AAA AAA CCT TTG GAA GTA	1110					
Pro Cys Ile Met His Phe Gln Val Leu Leu Lys Lys Pro Leu Glu Val						
105 110 115						

TTT	CGA	GCT	GAA	CTA	CTA	GTG	ACA	GAC	ATA	AAC	GAT	CAT	TCT	CCT	GAG	1158
Phe	Arg	Ala	Glu	Leu	Leu	Val	Thr	Asp	Ile	Asn	Asp	His	Ser	Pro	Glu	
			120					125					130			
TTT	CCT	GAA	AGA	GAA	ATG	ACC	CTG	AAA	ATC	CCA	GAA	ACT	AGC	TCC	CTT	1206
Phe	Pro	Glu	Arg	Glu	Met	Thr	Leu	Lys	Ile	Pro	Glu	Thr	Ser	Ser	Leu	
		135					140					145				
GGG	ACT	GTG	TTT	CCT	CTG	AAA	AAA	GCT	CGG	GAC	TTG	GAC	GTG	GGC	AGC	1254
Gly	Thr	Val	Phe	Pro	Leu	Lys	Lys	Ala	Arg	Asp	Leu	Asp	Val	Gly	Ser	
	150					155					160					
AAT	AAT	GTT	CAA	AAC	TAC	AAT	ATT	TCT	CCC	AAT	TCT	CAT	TTC	CAT	GTT	1302
Asn	Asn	Val	Gln	Asn	Tyr	Asn	Ile	Ser	Pro	Asn	Ser	His	Phe	His	Val	
165					170				175						180	
TCC	ACT	CGC	ACC	CGA	GGG	GAT	GGC	AGG	AAA	TAC	CCA	GAG	CTG	GTG	CTG	1350
Ser	Thr	Arg	Thr	Arg	Gly	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu	Val	Leu	
				185					190					195		
GAC	ACA	GAA	CTG	GAT	CGC	GAG	GAG	CAG	GCC	GAG	CTC	AGA	TTA	ACC	TTG	1398
Asp	Thr	Glu	Leu	Asp	Arg	Glu	Glu	Gln	Ala	Glu	Leu	Arg	Leu	Thr	Leu	
			200					205					210			
ACA	GCG	GTG	GAC	GGT	GGC	TCT	CCA	CCC	CGA	TCT	GGC	ACC	GTC	CAG	ATC	1446
Thr	Ala	Val	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	Thr	Val	Gln	Ile	
		215					220					225				
CTC	ATC	TTG	GTC	TTG	GAC	GCC	AAT	GAC	AAT	GCC	CCG	GAG	TTT	GTG	CAG	1494
Leu	Ile	Leu	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	Glu	Phe	Val	Gln	
	230					235					240					
GCG	CTC	TAC	GAG	GTG	CAG	GTC	CCA	GAG	AAC	AGC	CCA	GTA	GGC	TCC	CTA	1542
Ala	Leu	Tyr	Glu	Val	Gln	Val	Pro	Glu	Asn	Ser	Pro	Val	Gly	Ser	Leu	
	245				250					255					260	
GTT	GTC	AAG	GTC	TCT	GCT	AGG	GAT	TTA	GAC	ACT	GGG	ACA	AAT	GGA	GAG	1590
Val	Val	Lys	Val	Ser	Ala	Arg	Asp	Leu	Asp	Thr	Gly	Thr	Asn	Gly	Glu	
				265					270					275		
ATA	TCA	TAC	TCC	CTT	TAT	TAC	AGC	TCT	CAG	GAG	ATA	GAC	AAA	CCT	TTT	1638
Ile	Ser	Tyr	Ser	Leu	Tyr	Tyr	Ser	Ser	Gln	Glu	Ile	Asp	Lys	Pro	Phe	
			280					285					290			
GAG	CTA	AGC	AGC	CTT	TCA	GGA	GAA	ATT	CGA	CTA	ATT	AAA	AAA	CTA	GAT	1686
Glu	Leu	Ser	Ser	Leu	Ser	Gly	Glu	Ile	Arg	Leu	Ile	Lys	Lys	Leu	Asp	
		295					300					305				
TTT	GAG	ACA	ATG	TCT	TCA	TAT	GAT	CTA	GAT	ATA	GAG	GCA	TCT	GAT	GGC	1734
Phe	Glu	Thr	Met	Ser	Ser	Tyr	Asp	Leu	Asp	Ile	Glu	Ala	Ser	Asp	Gly	
	310					315					320					
GGG	GGA	CTT	TCT	GGA	AAA	TGC	TCT	GTC	TCT	GTT	AAG	GTG	CTG	GAT	GTT	1782
Gly	Gly	Leu	Ser	Gly	Lys	Cys	Ser	Val	Ser	Val	Lys	Val	Leu	Asp	Val	
	325				330					335					340	
AAC	GAT	AAC	TTC	CCG	GAA	CTA	AGT	ATT	TCA	TCA	CTT	ACC	AGC	CCT	ATT	1830
Asn	Asp	Asn	Phe	Pro	Glu	Leu	Ser	Ile	Ser	Ser	Leu	Thr	Ser	Pro	Ile	
				345					350					355		

CCC Pro	GAG Glu	AAT Asn	TCT Ser	CCA Pro	GAG Glu	ACA Thr	GAA Glu	GTG Val	GCC Ala	CTG Leu	TTT Phe	AGG Arg	ATT Ile	AGA Arg	GAC Asp	1878
		360						365					370			
CGA Arg	GAC Asp	TCT Ser	GGA Gly	GAA Glu	AAT Asn	GGA Gly	AAA Lys	ATG Met	ATT Ile	TGC Cys	TCA Ser	ATT Ile	CAG Gln	GAT Asp	GAT Asp	1926
		375					380					385				
GTT Val	CCT Pro	TTT Phe	AAG Lys	CTA Leu	AAA Lys	CCT Pro	TCT Ser	GTT Val	GAG Glu	AAT Asn	TTC Phe	TAC Tyr	AGG Arg	CTG Leu	GTA Val	1974
	390					395					400					
ACA Thr	GAA Glu	GGG Gly	GCG Ala	CTG Leu	GAC Asp	AGA Arg	GAG Glu	ACC Thr	AGA Arg	GCC Ala	GAG Glu	TAC Tyr	AAC Asn	ATC Ile	ACC Thr	2022
	405				410					415					420	
ATC Ile	ACC Thr	ATC Ile	ACA Thr	GAC Asp	TTG Leu	GGG Gly	ACT Thr	CCA Pro	AGG Arg	CTG Leu	AAA Lys	ACC Thr	GAG Glu	CAG Gln	AGC Ser	2070
				425				430						435		
ATA Ile	ACC Thr	GTG Val	CTG Leu	GTG Val	TCG Ser	GAC Asp	GTC Val	AAT Asn	GAC Asp	AAC Asn	GCC Ala	CCC Pro	GCC Ala	TTC Phe	ACC Thr	2118
			440				445						450			
CAA Gln	ACC Thr	TCC Ser	TAC Tyr	ACC Thr	CTG Leu	TTC Phe	GTC Val	CGC Arg	GAG Glu	AAC Asn	AAC Asn	AGC Ser	CCC Pro	GCC Ala	CTG Leu	2166
		455					460					465				
CAC His	ATC Ile	GGC Gly	AGT Ser	GTC Val	AGC Ser	GCC Ala	ACA Thr	GAC Asp	AGA Arg	GAC Asp	TCG Ser	GGC Gly	ACC Thr	AAC Asn	GCC Ala	2214
	470					475					480					
CAG Gln	GTC Val	ACC Thr	TAC Tyr	TCG Ser	CTG Leu	CTG Leu	CCG Pro	CCC Pro	CAG Gln	GAC Asp	CCG Pro	CAC His	CTG Leu	CCC Pro	CTA Leu	2262
	485				490				495						500	
ACC Thr	TCC Ser	CTG Leu	GTC Val	TCC Ser	ATT Ile	AAC Asn	ACG Thr	GAC Asp	AAC Asn	GGC Gly	CAC His	CTG Leu	TTC Phe	GCT Ala	CTC Leu	2310
				505					510					515		
CAG Gln	TCG Ser	CTG Leu	GAC Asp	TAC Tyr	GAG Glu	GCC Ala	CTG Leu	CAG Gln	GCT Ala	TTC Phe	GAG Glu	TTC Phe	CGC Arg	GTG Val	GGC Gly	2358
			520					525					530			
GCC Ala	ACA Thr	GAC Asp	CGC Arg	GGC Gly	TTC Phe	CCG Pro	GCG Ala	CTG Leu	AGC Ser	AGC Ser	GAG Glu	GCG Ala	CTG Leu	GTG Val	CGA Arg	2406
		535					540					545				
GTG Val	CTG Leu	GTG Val	CTG Leu	GAC Asp	GCC Ala	AAC Asn	GAC Asp	AAC Asn	TCG Ser	CCC Pro	TTC Phe	GTG Val	CTG Leu	TAC Tyr	CCG Pro	2454
		550				555					560					
CTG Leu	CAG Gln	AAC Asn	GGC Gly	TCC Ser	GCG Ala	CCC Pro	TGC Cys	ACC Thr	GAG Glu	CTG Leu	GTG Val	CCC Pro	CGG Arg	GCG Ala	GCC Ala	2502
	565				570					575					580	
GAG Glu	CCG Pro	GGC Gly	TAC Tyr	CTG Leu	GTG Val	ACC Thr	AAG Lys	GTG Val	GTG Val	GCG Ala	GTG Val	GAC Asp	GGC Gly	GAC Asp	TCG Ser	2550
				585					590					595		

GGC CAG AAC GCC TGG CTG TCG TAC CAG CTG CTC AAG GCC ACG GAG CCC	2598
Gly Gln Asn Ala Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Pro	
600 605 610	
GGG CTG TTC GGC GTG TGG GCG CAC AAT GGC GAG GTG CGC ACC GCC AGG	2646
Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg	
615 620 625	
CTG CTG AGC GAG CGC GAC GTG GCC AAG CAC AGG CTA GTG GTG CTG GTC	2694
Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu Val Val Leu Val	
630 635 640	
AAG GAC AAT GGC GAG CCT CCG CGC TCG GCC ACA GCC ACG CTG CAA GTG	2742
Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu Gln Val	
645 650 655 660	
CTC CTG GTG GAC GGC TTC TCT CAG CCC TAC CTG CCG CTC CCA GAG GCG	2790
Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu Ala	
665 670 675	
GCC CCG GCC CAA GCC CAG GCC GAC TCG CTT ACC GTC TAC CTG GTG GTG	2838
Ala Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val Tyr Leu Val Val	
680 685 690	
GCA TTG GCC TCG GTG TCT TCG CTC TTC CTC TTC TCG GTG TTC CTG TTC	2886
Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val Phe Leu Phe	
695 700 705	
GTG GCA GTG CGG CTG TGC AGG AGG AGC AGG GCG GCC TCA GTG GGT CGC	2934
Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala Ser Val Gly Arg	
710 715 720	
TGC TCG GTG CCC GAG GGC CCC TTT CCA GGG CAT CTG GTG GAC GTG AGC	2982
Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu Val Asp Val Ser	
725 730 735 740	
GGC ACC GGG ACC CTT TCC CAG AGC TAC CAG TAC GAG GTG TGT CTG ACG	3030
Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu Val Cys Leu Thr	
745 750 755	
GGA GGC TCT GAA AGT AAT GAT TTC AAG TTC TTG AAG CCT ATA TTC CCA	3078
Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys Pro Ile Phe Pro	
760 765 770	
AAT ATT GTA AGC CAG GAC TCT AGG AGG AAA TCA GAA TTT CTA GAA	3123
Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu Phe Leu Glu	
775 780 785	
TAATGTAGGT ATCTGTAGCT TTCCGACCGT CTGTTAATTT TGTCTTCCTC ACTTTTCACC	3183
TTAGTTTTTT TTAACCCTTT AGTAATCTTG AATTCTACTT TTTTTTAAAT TTCTACTGTT	3243
GTCTTTAGTA ATGTTACTCA TTTCTTTTGT CTGATTGTGA GTTTTCAAAT TATTGTATTA	3303
TTATAAATAT TTTATATCAG GAAAGTTCAT ATTTCTGAAT AAATTAATAG	3353

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met	Glu	Pro	Ala	Gly	Glu	Arg	Phe	Pro	Glu	Gln	Arg	Gln	Val	Leu	Ile	
1				5					10					15		
Leu	Leu	Leu	Leu	Leu	Glu	Val	Thr	Leu	Ala	Gly	Trp	Glu	Pro	Arg	Arg	
			20					25					30			
Tyr	Ser	Val	Met	Glu	Glu	Thr	Glu	Arg	Gly	Ser	Phe	Val	Ala	Asn	Leu	
		35					40					45				
Ala	Asn	Asp	Leu	Gly	Leu	Gly	Val	Gly	Glu	Leu	Ala	Glu	Arg	Gly	Ala	
	50					55					60					
Arg	Val	Val	Ser	Glu	Asp	Asn	Glu	Gln	Gly	Leu	Gln	Leu	Asp	Leu	Gln	
65					70					75					80	
Thr	Gly	Gln	Leu	Ile	Leu	Asn	Glu	Lys	Leu	Asp	Arg	Glu	Lys	Leu	Cys	
			85						90					95		
Gly	Pro	Thr	Glu	Pro	Cys	Ile	Met	His	Phe	Gln	Val	Leu	Leu	Lys	Lys	
			100					105					110			
Pro	Leu	Glu	Val	Phe	Arg	Ala	Glu	Leu	Leu	Val	Thr	Asp	Ile	Asn	Asp	
		115					120					125				
His	Ser	Pro	Glu	Phe	Pro	Glu	Arg	Glu	Met	Thr	Leu	Lys	Ile	Pro	Glu	
	130					135					140					
Thr	Ser	Ser	Leu	Gly	Thr	Val	Phe	Pro	Leu	Lys	Lys	Ala	Arg	Asp	Leu	
145					150					155					160	
Asp	Val	Gly	Ser	Asn	Asn	Val	Gln	Asn	Tyr	Asn	Ile	Ser	Pro	Asn	Ser	
				165					170					175		
His	Phe	His	Val	Ser	Thr	Arg	Thr	Arg	Gly	Asp	Gly	Arg	Lys	Tyr	Pro	
			180					185					190			
Glu	Leu	Val	Leu	Asp	Thr	Glu	Leu	Asp	Arg	Glu	Glu	Gln	Ala	Glu	Leu	
		195					200					205				
Arg	Leu	Thr	Leu	Thr	Ala	Val	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	
	210					215					220					
Thr	Val	Gln	Ile	Leu	Ile	Leu	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	
225					230					235					240	
Glu	Phe	Val	Gln	Ala	Leu	Tyr	Glu	Val	Gln	Val	Pro	Glu	Asn	Ser	Pro	
				245					250				255			
Val	Gly	Ser	Leu	Val	Val	Lys	Val	Ser	Ala	Arg	Asp	Leu	Asp	Thr	Gly	
			260					265					270			
Thr	Asn	Gly	Glu	Ile	Ser	Tyr	Ser	Leu	Tyr	Tyr	Ser	Ser	Gln	Glu	Ile	
		275					280					285				

Asp	Lys	Pro	Phe	Glu	Leu	Ser	Ser	Leu	Ser	Gly	Glu	Ile	Arg	Leu	Ile	290	295	300	
Lys	Lys	Leu	Asp	Phe	Glu	Thr	Met	Ser	Ser	Tyr	Asp	Leu	Asp	Ile	Glu	305	310	315	320
Ala	Ser	Asp	Gly	Gly	Gly	Leu	Ser	Gly	Lys	Cys	Ser	Val	Ser	Val	Lys	325	330	335	
Val	Leu	Asp	Val	Asn	Asp	Asn	Phe	Pro	Glu	Leu	Ser	Ile	Ser	Ser	Leu	340	345	350	
Thr	Ser	Pro	Ile	Pro	Glu	Asn	Ser	Pro	Glu	Thr	Glu	Val	Ala	Leu	Phe	355	360	365	
Arg	Ile	Arg	Asp	Arg	Asp	Ser	Gly	Glu	Asn	Gly	Lys	Met	Ile	Cys	Ser	370	375	380	
Ile	Gln	Asp	Asp	Val	Pro	Phe	Lys	Leu	Lys	Pro	Ser	Val	Glu	Asn	Phe	385	390	395	400
Tyr	Arg	Leu	Val	Thr	Glu	Gly	Ala	Leu	Asp	Arg	Glu	Thr	Arg	Ala	Glu	405	410	415	
Tyr	Asn	Ile	Thr	Ile	Thr	Ile	Thr	Asp	Leu	Gly	Thr	Pro	Arg	Leu	Lys	420	425	430	
Thr	Glu	Gln	Ser	Ile	Thr	Val	Leu	Val	Ser	Asp	Val	Asn	Asp	Asn	Ala	435	440	445	
Pro	Ala	Phe	Thr	Gln	Thr	Ser	Tyr	Thr	Leu	Phe	Val	Arg	Glu	Asn	Asn	450	455	460	
Ser	Pro	Ala	Leu	His	Ile	Gly	Ser	Val	Ser	Ala	Thr	Asp	Arg	Asp	Ser	465	470	475	480
Gly	Thr	Asn	Ala	Gln	Val	Thr	Tyr	Ser	Leu	Leu	Pro	Pro	Gln	Asp	Pro	485	490	495	
His	Leu	Pro	Leu	Thr	Ser	Leu	Val	Ser	Ile	Asn	Thr	Asp	Asn	Gly	His	500	505	510	
Leu	Phe	Ala	Leu	Gln	Ser	Leu	Asp	Tyr	Glu	Ala	Leu	Gln	Ala	Phe	Glu	515	520	525	
Phe	Arg	Val	Gly	Ala	Thr	Asp	Arg	Gly	Phe	Pro	Ala	Leu	Ser	Ser	Glu	530	535	540	
Ala	Leu	Val	Arg	Val	Leu	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ser	Pro	Phe	545	550	555	560
Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	Pro	Cys	Thr	Glu	Leu	Val	565	570	575	
Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	580	585	590	
Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	595	600	605	

Ala Thr Glu Pro Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val
610 615 620

Arg Thr Ala Arg Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu
625 630 635 640

Val Val Leu Val Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala
645 650 655

Thr Leu Gln Val Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro
660 665 670

Leu Pro Glu Ala Ala Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val
675 680 685

Tyr Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser
690 695 700

Val Phe Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala
705 710 715 720

Ser Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu
725 730 735

Val Asp Val Ser Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu
740 745 750

Val Cys Leu Thr Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys
755 760 765

Pro Ile Phe Pro Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu
770 775 780

Phe Leu Glu
785

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3033 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 138..2528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GTGATTGGAC GTGTTTTTGT GACTATTTGG GAAGAAGACA CCTTCCTAAT CAGATTTACT	60
CCAATATCTT CCCGGACCCT CATGAGTGGA TTGCAATTGA CTTGAAGAAG CAGCACCTC	120
AGGACTGAAT CTGAACA ATG GAG ACA GCA CTA GCA AAA ATA CCA CAG CAA	170
Met Glu Thr Ala Leu Ala Lys Ile Pro Gln Gln	
1 5 10	

AGG	CAA	GTC	TTT	TTT	CTT	ACT	ATA	TTG	TCG	TTA	TTG	TGG	AAG	TCT	AGC	218
Arg	Gln	Val	Phe	Phe	Leu	Thr	Ile	Leu	Ser	Leu	Leu	Trp	Lys	Ser	Ser	
			15					20					25			
TCT	GAG	GCC	ATT	AGA	TAT	TCC	ATG	CCA	GAA	GAA	ACA	GAG	AGT	GGC	TAT	266
Ser	Glu	Ala	Ile	Arg	Tyr	Ser	Met	Pro	Glu	Glu	Thr	Glu	Ser	Gly	Tyr	
		30					35					40				
ATG	GTG	GCT	AAC	CTG	GCG	AAA	GAT	CTG	GGG	ATC	AGG	GTT	GGA	GAA	CTG	314
Met	Val	Ala	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Ile	Arg	Val	Gly	Glu	Leu	
	45					50					55					
TCC	TCT	AGA	GGA	GCT	CAA	ATC	CAT	TAC	AAA	GGA	AAC	AAA	GAA	CTT	TTG	362
Ser	Ser	Arg	Gly	Ala	Gln	Ile	His	Tyr	Lys	Gly	Asn	Lys	Glu	Leu	Leu	
	60				65					70					75	
CAG	CTG	GAT	GCA	GAG	ACT	GGG	AAT	TTG	TTC	TTA	AAG	GAA	AAA	CTA	GAC	410
Gln	Leu	Asp	Ala	Glu	Thr	Gly	Asn	Leu	Phe	Leu	Lys	Glu	Lys	Leu	Asp	
				80					85					90		
AGA	GAA	CTG	CTG	TGT	GGA	GAG	ACA	GAA	CCC	TGT	GTG	CTG	AAC	TTC	CAG	458
Arg	Glu	Leu	Leu	Cys	Gly	Glu	Thr	Glu	Pro	Cys	Val	Leu	Asn	Phe	Gln	
			95					100					105			
ATC	ATA	CTG	GAA	AAC	CCT	ATG	CAG	TTC	TTC	CAA	ACT	GAA	CTG	CAG	CTC	506
Ile	Ile	Leu	Glu	Asn	Pro	Met	Gln	Phe	Phe	Gln	Thr	Glu	Leu	Gln	Leu	
		110					115					120				
ACA	GAT	ATA	AAC	GAC	CAT	TCT	CCA	GAG	TTC	CCC	AAC	AAG	AAA	ATG	CTT	554
Thr	Asp	Ile	Asn	Asp	His	Ser	Pro	Glu	Phe	Pro	Asn	Lys	Lys	Met	Leu	
	125					130					135					
CTA	ACA	ATT	CCT	GAG	AGT	GCC	CAT	CCA	GGG	ACT	GTG	TTT	CCT	CTG	AAG	602
Leu	Thr	Ile	Pro	Glu	Ser	Ala	His	Pro	Gly	Thr	Val	Phe	Pro	Leu	Lys	
	140					145				150					155	
GCA	GCT	CGG	GAC	TCT	GAC	ATA	GGG	AGC	AAC	GCT	GTT	CAG	AAC	TAC	ACA	650
Ala	Ala	Arg	Asp	Ser	Asp	Ile	Gly	Ser	Asn	Ala	Val	Gln	Asn	Tyr	Thr	
				160					165					170		
GTC	AAT	CCC	AAC	CTC	CAT	TTC	CAC	GTC	GTT	ACT	CAC	AGT	CGC	ACA	GAT	698
Val	Asn	Pro	Asn	Leu	His	Phe	His	Val	Val	Thr	His	Ser	Arg	Thr	Asp	
			175					180					185			
GGC	AGG	AAA	TAC	CCA	GAG	CTG	GTG	CTG	GAC	AGA	GCC	CTG	GAT	AGG	GAG	746
Gly	Arg	Lys	Tyr	Pro	Glu	Leu	Val	Leu	Asp	Arg	Ala	Leu	Asp	Arg	Glu	
		190					195					200				
GAG	CAG	CCT	GAG	CTC	ACT	TTA	ATC	CTC	ACT	GCT	CTG	GAT	GGT	GGA	GCT	794
Glu	Gln	Pro	Glu	Leu	Thr	Leu	Ile	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ala	
	205					210					215					
CCT	TCC	AGG	TCA	GGA	ACC	ACC	ACA	GTT	CAC	ATA	GAA	GTT	GTG	GAC	ATC	842
Pro	Ser	Arg	Ser	Gly	Thr	Thr	Thr	Val	His	Ile	Glu	Val	Val	Asp	Ile	
	220				225					230					235	
AAT	GAT	AAC	TCC	CCC	CAG	TTT	GTA	CAG	TCA	CTC	TAT	AAG	GTG	CAA	GTT	890
Asn	Asp	Asn	Ser	Pro	Gln	Phe	Val	Gln	Ser	Leu	Tyr	Lys	Val	Gln	Val	
				240					245					250		

CCT	GAG	AAT	AAT	CCC	CTC	AAT	GCC	TTT	GTT	GTC	ACG	GTC	TCT	GCC	ACG	938
Pro	Glu	Asn	Asn	Pro	Leu	Asn	Ala	Phe	Val	Val	Thr	Val	Ser	Ala	Thr	
		255						260					265			
GAT	TTA	GAT	GCT	GGG	GTA	TAT	GGC	AAT	GTG	ACC	TAT	TCT	CTG	TTT	CAA	986
Asp	Leu	Asp	Ala	Gly	Val	Tyr	Gly	Asn	Val	Thr	Tyr	Ser	Leu	Phe	Gln	
		270					275					280				
GGG	TAT	GGG	GTA	TTT	CAA	CCA	TTT	GTA	ATA	GAC	GAA	ATC	ACT	GGA	GAA	1034
Gly	Tyr	Gly	Val	Phe	Gln	Pro	Phe	Val	Ile	Asp	Glu	Ile	Thr	Gly	Glu	
	285					290					295					
ATC	CAT	CTG	AGC	AAA	GAG	CTG	GAT	TTT	GAG	GAA	ATT	AGC	AAT	CAT	AAC	1082
Ile	His	Leu	Ser	Lys	Glu	Leu	Asp	Phe	Glu	Glu	Ile	Ser	Asn	His	Asn	
300					305					310					315	
ATA	GAA	ATC	GCA	GCC	ACA	GAT	GGA	GGA	GGC	CTT	TCA	GGA	AAA	TGC	ACT	1130
Ile	Glu	Ile	Ala	Ala	Thr	Asp	Gly	Gly	Gly	Leu	Ser	Gly	Lys	Cys	Thr	
				320					325					330		
GTG	GCT	GTA	CAG	GTG	TTG	GAT	GTG	AAT	GAC	AAC	GCC	CCA	GAG	TTG	ACA	1178
Val	Ala	Val	Gln	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro	Glu	Leu	Thr	
			335					340					345			
ATT	AGG	AAG	CTC	ACA	GTC	CTG	GTC	CCA	GAA	AAT	TCC	GCA	GAG	ACT	GTA	1226
Ile	Arg	Lys	Leu	Thr	Val	Leu	Val	Pro	Glu	Asn	Ser	Ala	Glu	Thr	Val	
		350					355					360				
GTT	GCT	GTT	TTT	AGT	GTT	TCT	GAT	TCT	GAT	TCG	GGG	GAC	AAT	GGA	AGG	1274
Val	Ala	Val	Phe	Ser	Val	Ser	Asp	Ser	Asp	Ser	Gly	Asp	Asn	Gly	Arg	
	365					370					375					
ATG	GTG	TGT	TCT	ATT	CCG	AAC	AAT	ATC	CCA	TTT	CTC	CTG	AAA	CCC	ACA	1322
Met	Val	Cys	Ser	Ile	Pro	Asn	Asn	Ile	Pro	Phe	Leu	Leu	Lys	Pro	Thr	
380					385				390						395	
TTT	GAG	AAT	TAT	TAC	ACG	TTA	GTG	ACT	GAG	GGG	CCA	CTT	GAT	AGA	GAG	1370
Phe	Glu	Asn	Tyr	Tyr	Thr	Leu	Val	Thr	Glu	Gly	Pro	Leu	Asp	Arg	Glu	
			400						405					410		
AAC	AGA	GCT	GAG	TAC	AAC	ATC	ACC	ATC	ACG	GTC	TCA	GAT	CTG	GGC	ACA	1418
Asn	Arg	Ala	Glu	Tyr	Asn	Ile	Thr	Ile	Thr	Val	Ser	Asp	Leu	Gly	Thr	
			415					420					425			
CCC	AGG	CTC	ACA	ACC	CAG	CAC	ACC	ATA	ACA	GTG	CAA	GTG	TCC	GAC	ATC	1466
Pro	Arg	Leu	Thr	Thr	Gln	His	Thr	Ile	Thr	Val	Gln	Val	Ser	Asp	Ile	
		430					435					440				
AAC	GAC	AAC	GCC	CCT	GCC	TTC	ACC	CAA	ACC	TCC	TAC	ACC	ATG	TTT	GTC	1514
Asn	Asp	Asn	Ala	Pro	Ala	Phe	Thr	Gln	Thr	Ser	Tyr	Thr	Met	Phe	Val	
	445					450					455					
CAC	GAG	AAC	AAC	AGC	CCC	GCC	CTG	CAC	ATA	GGC	ACC	ATC	AGT	GCC	ACA	1562
His	Glu	Asn	Asn	Ser	Pro	Ala	Leu	His	Ile	Gly	Thr	Ile	Ser	Ala	Thr	
460					465					470					475	
GAC	TCA	GAC	TCA	GGC	TCC	AAT	GCC	CAC	ATC	ACC	TAC	TCG	CTG	CTG	CCG	1610
Asp	Ser	Asp	Ser	Gly	Ser	Asn	Ala	His	Ile	Thr	Tyr	Ser	Leu	Leu	Pro	
				480					485						490	

CCT	GAT	GAC	CCG	CAG	CTG	GCC	CTC	GAC	TCA	CTC	ATC	TCC	ATC	AAT	GTT	1658
Pro	Asp	Asp	Pro	Gln	Leu	Ala	Leu	Asp	Ser	Leu	Ile	Ser	Ile	Asn	Val	
			495					500					505			
GAC	AAT	GGG	CAG	CTG	TTC	GCG	CTC	AGA	GCT	CTA	GAC	TAT	GAG	GCA	CTG	1706
Asp	Asn	Gly	Gln	Leu	Phe	Ala	Leu	Arg	Ala	Leu	Asp	Tyr	Glu	Ala	Leu	
		510					515					520				
CAG	TCC	TTC	GAG	TTC	TAC	GTG	GGC	GCT	ACA	GAT	GGA	GGC	TCA	CCC	GCG	1754
Gln	Ser	Phe	Glu	Phe	Tyr	Val	Gly	Ala	Thr	Asp	Gly	Gly	Ser	Pro	Ala	
	525					530					535					
CTC	AGC	AGC	CAG	ACT	CTG	GTG	CGG	ATG	GTG	GTG	CTG	GAT	GAC	AAT	GAC	1802
Leu	Ser	Ser	Gln	Thr	Leu	Val	Arg	Met	Val	Val	Leu	Asp	Asp	Asn	Asp	
540					545				550						555	
AAT	GCC	CCC	TTC	GTG	CTC	TAC	CCA	CTG	CAG	AAT	GCC	TCA	GCA	CCC	TGT	1850
Asn	Ala	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Ala	Ser	Ala	Pro	Cys	
			560					565						570		
ACT	GAG	CTA	CTG	CCT	AGG	GCA	GCA	GAG	CCC	GGC	TAC	CTG	ATC	ACC	AAA	1898
Thr	Glu	Leu	Leu	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	Ile	Thr	Lys	
			575					580					585			
GTG	GTG	GCT	GTG	GAT	CGC	GAC	TCT	GGA	CAG	AAT	GCT	TGG	CTG	TCG	TTC	1946
Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	Asn	Ala	Trp	Leu	Ser	Phe	
		590					595					600				
CAG	CTA	CTT	AAA	GCT	ACA	GAG	CCA	GGG	CTG	TTC	AGT	GTA	TGG	GCA	CAC	1994
Gln	Leu	Leu	Lys	Ala	Thr	Glu	Pro	Gly	Leu	Phe	Ser	Val	Trp	Ala	His	
	605					610					615					
AAT	GGT	GAA	GTG	CGC	ACC	ACT	AGG	CTG	CTG	AGT	GAG	CGA	GAT	GCT	CAG	2042
Asn	Gly	Glu	Val	Arg	Thr	Thr	Arg	Leu	Leu	Ser	Glu	Arg	Asp	Ala	Gln	
620					625					630					635	
AAG	CAC	AAG	CTA	CTG	CTG	CTG	GTC	AAG	GAC	AAT	GGC	GAT	CCT	CTG	CGC	2090
Lys	His	Lys	Leu	Leu	Leu	Leu	Val	Lys	Asp	Asn	Gly	Asp	Pro	Leu	Arg	
			640						645					650		
TCT	GCC	AAT	GTC	ACT	CTT	CAC	GTG	CTA	GTG	GTG	GAT	GGC	TTC	TCG	CAG	2138
Ser	Ala	Asn	Val	Thr	Leu	His	Val	Leu	Val	Val	Asp	Gly	Phe	Ser	Gln	
			655					660					665			
CCT	TAC	CTA	CCA	TTG	GCT	GAG	GTG	GCA	CAG	GAT	TCC	ATG	CAA	GAT	AAT	2186
Pro	Tyr	Leu	Pro	Leu	Ala	Glu	Val	Ala	Gln	Asp	Ser	Met	Gln	Asp	Asn	
		670					675					680				
TAC	GAC	GTT	CTC	ACA	CTG	TAC	CTA	GTC	ATT	GCC	TTG	GCA	TCT	GTA	TCT	2234
Tyr	Asp	Val	Leu	Thr	Leu	Tyr	Leu	Val	Ile	Ala	Leu	Ala	Ser	Val	Ser	
	685					690					695					
TCT	CTC	TTC	CTC	TTG	TCT	GTA	GTG	CTG	TTT	GTG	GGG	GTG	AGG	CTG	TGC	2282
Ser	Leu	Phe	Leu	Leu	Ser	Val	Val	Leu	Phe	Val	Gly	Val	Arg	Leu	Cys	
700					705					710					715	
AGG	AGG	GCC	AGG	GAG	GCC	TCC	TTG	GGT	GAC	TAC	TCT	GTG	CCT	GAG	GGA	2330
Arg	Arg	Ala	Arg	Glu	Ala	Ser	Leu	Gly	Asp	Tyr	Ser	Val	Pro	Glu	Gly	
				720					725					730		
CAC	TTT	CCT	AGC	CAC	TTG	GTG	GAT	GTC	AGC	GGT	GCC	GGG	ACC	CTG	TCC	2378

His	Phe	Pro	Ser	His	Leu	Val	Asp	Val	Ser	Gly	Ala	Gly	Thr	Leu	Ser		
			735					740					745				
CAG	AGT	TAT	CAA	TAT	GAG	GTG	TGT	CTT	AAT	GGA	GGT	ACT	AGA	ACA	AAT		2426
Gln	Ser	Tyr	Gln	Tyr	Glu	Val	Cys	Leu	Asn	Gly	Gly	Thr	Arg	Thr	Asn		
		750					755					760					
GAG	TTT	AAC	TTT	CTT	AAA	CCA	TTG	TTT	CCT	ATC	CTT	CCG	ACC	CAG	GCT		2474
Glu	Phe	Asn	Phe	Leu	Lys	Pro	Leu	Phe	Pro	Ile	Leu	Pro	Thr	Gln	Ala		
	765					770					775						
GCT	GCT	GCT	GAA	GAA	AGA	GAA	AAC	GCT	GTT	GTG	CAC	AAT	AGC	GTT	GGA		2522
Ala	Ala	Ala	Glu	Glu	Arg	Glu	Asn	Ala	Val	Val	His	Asn	Ser	Val	Gly		
780					785				790					795			
TTC	TAT	TAGAGCACTG	ATTTTGAAGT	GGTGGTTACC	TCATTTTTC	TTAACTATCC											2578
Phe	Tyr																
CTGATGTAGA	ATGGTGTAGT	GCCGTGAATC	AACTCCTGAG	ATATATGTTT	ATTTTATCCT												2638
TTGTTTTGAA	TCAAACCTATT	CAGATGTGAT	CCTACTCTAG	AGAATTTGGT	TCTACTCCAT												2698
TGTGTTTGT	TAGATTTCTA	CGCCATACCA	GTGCATGCTG	GGTTGTTTTT	TTTTTTACAA												2758
TTATTATAAC	TTTGCTTTGG	AGGGGAACTC	ATATTCGCTG	TAACGAATTG	GAACCACTTT												2818
CATTGTTAGA	GATGCCTTGC	TTTGTGTGT	TATTTTCAGAC	AGGGTCTTAA	ATTGTAGCCC												2878
TGGGTGACCT	GAAATGACTA	TGTACAGACT	GACTTTGAAT	TTGTGGCAGT	CCATCTGCCT												2938
CTGTTGTCCT	ATGTTGGGAT	TGTGAGCATG	CATGAGTAGG	CTCAGCTGTG	GTGAGCGACC												2998
TTAATAAAAA	TCAAATACTA	AAAAAAAAAA	AAAAA														3033

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Glu	Thr	Ala	Leu	Ala	Lys	Ile	Pro	Gln	Gln	Arg	Gln	Val	Phe	Phe		
1				5				10						15			
Leu	Thr	Ile	Leu	Ser	Leu	Leu	Trp	Lys	Ser	Ser	Ser	Glu	Ala	Ile	Arg		
			20					25					30				
Tyr	Ser	Met	Pro	Glu	Glu	Thr	Glu	Ser	Gly	Tyr	Met	Val	Ala	Asn	Leu		
		35				40						45					
Ala	Lys	Asp	Leu	Gly	Ile	Arg	Val	Gly	Glu	Leu	Ser	Ser	Arg	Gly	Ala		
	50				55						60						
Gln	Ile	His	Tyr	Lys	Gly	Asn	Lys	Glu	Leu	Leu	Gln	Leu	Asp	Ala	Glu		
65					70					75					80		

Thr Gly Asn Leu Phe Leu Lys Glu Lys Leu Asp Arg Glu Leu Leu Cys
85 90 95

Gly Glu Thr Glu Pro Cys Val Leu Asn Phe Gln Ile Ile Leu Glu Asn
100 105 110

Pro Met Gln Phe Phe Gln Thr Glu Leu Gln Leu Thr Asp Ile Asn Asp
115 120 125

His Ser Pro Glu Phe Pro Asn Lys Lys Met Leu Leu Thr Ile Pro Glu
130 135 140

Ser Ala His Pro Gly Thr Val Phe Pro Leu Lys Ala Ala Arg Asp Ser
145 150 155 160

Asp Ile Gly Ser Asn Ala Val Gln Asn Tyr Thr Val Asn Pro Asn Leu
165 170 175

His Phe His Val Val Thr His Ser Arg Thr Asp Gly Arg Lys Tyr Pro
180 185 190

Glu Leu Val Leu Asp Arg Ala Leu Asp Arg Glu Glu Gln Pro Glu Leu
195 200 205

Thr Leu Ile Leu Thr Ala Leu Asp Gly Gly Ala Pro Ser Arg Ser Gly
210 215 220

Thr Thr Thr Val His Ile Glu Val Val Asp Ile Asn Asp Asn Ser Pro
225 230 235 240

Gln Phe Val Gln Ser Leu Tyr Lys Val Gln Val Pro Glu Asn Asn Pro
245 250 255

Leu Asn Ala Phe Val Val Thr Val Ser Ala Thr Asp Leu Asp Ala Gly
260 265 270

Val Tyr Gly Asn Val Thr Tyr Ser Leu Phe Gln Gly Tyr Gly Val Phe
275 280 285

Gln Pro Phe Val Ile Asp Glu Ile Thr Gly Glu Ile His Leu Ser Lys
290 295 300

Glu Leu Asp Phe Glu Glu Ile Ser Asn His Asn Ile Glu Ile Ala Ala
305 310 315 320

Thr Asp Gly Gly Gly Leu Ser Gly Lys Cys Thr Val Ala Val Gln Val
325 330 335

Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Thr Ile Arg Lys Leu Thr
340 345 350

Val Leu Val Pro Glu Asn Ser Ala Glu Thr Val Val Ala Val Phe Ser
355 360 365

Val Ser Asp Ser Asp Ser Gly Asp Asn Gly Arg Met Val Cys Ser Ile
370 375 380

Pro Asn Asn Ile Pro Phe Leu Leu Lys Pro Thr Phe Glu Asn Tyr Tyr
385 390 395 400

Thr	Leu	Val	Thr	Glu	Gly	Pro	Leu	Asp	Arg	Glu	Asn	Arg	Ala	Glu	Tyr	405	410	415
Asn	Ile	Thr	Ile	Thr	Val	Ser	Asp	Leu	Gly	Thr	Pro	Arg	Leu	Thr	Thr	420	425	430
Gln	His	Thr	Ile	Thr	Val	Gln	Val	Ser	Asp	Ile	Asn	Asp	Asn	Ala	Pro	435	440	445
Ala	Phe	Thr	Gln	Thr	Ser	Tyr	Thr	Met	Phe	Val	His	Glu	Asn	Asn	Ser	450	455	460
Pro	Ala	Leu	His	Ile	Gly	Thr	Ile	Ser	Ala	Thr	Asp	Ser	Asp	Ser	Gly	465	470	475
Ser	Asn	Ala	His	Ile	Thr	Tyr	Ser	Leu	Leu	Pro	Pro	Asp	Asp	Pro	Gln	485	490	495
Leu	Ala	Leu	Asp	Ser	Leu	Ile	Ser	Ile	Asn	Val	Asp	Asn	Gly	Gln	Leu	500	505	510
Phe	Ala	Leu	Arg	Ala	Leu	Asp	Tyr	Glu	Ala	Leu	Gln	Ser	Phe	Glu	Phe	515	520	525
Tyr	Val	Gly	Ala	Thr	Asp	Gly	Gly	Ser	Pro	Ala	Leu	Ser	Ser	Gln	Thr	530	535	540
Leu	Val	Arg	Met	Val	Val	Leu	Asp	Asp	Asn	Asp	Asn	Ala	Pro	Phe	Val	545	550	555
Leu	Tyr	Pro	Leu	Gln	Asn	Ala	Ser	Ala	Pro	Cys	Thr	Glu	Leu	Leu	Pro	565	570	575
Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	Ile	Thr	Lys	Val	Val	Ala	Val	Asp	580	585	590
Arg	Asp	Ser	Gly	Gln	Asn	Ala	Trp	Leu	Ser	Phe	Gln	Leu	Leu	Lys	Ala	595	600	605
Thr	Glu	Pro	Gly	Leu	Phe	Ser	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	610	615	620
Thr	Thr	Arg	Leu	Leu	Ser	Glu	Arg	Asp	Ala	Gln	Lys	His	Lys	Leu	Leu	625	630	635
Leu	Leu	Val	Lys	Asp	Asn	Gly	Asp	Pro	Leu	Arg	Ser	Ala	Asn	Val	Thr	645	650	655
Leu	His	Val	Leu	Val	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	660	665	670
Ala	Glu	Val	Ala	Gln	Asp	Ser	Met	Gln	Asp	Asn	Tyr	Asp	Val	Leu	Thr	675	680	685
Leu	Tyr	Leu	Val	Ile	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Leu	690	695	700
Ser	Val	Val	Leu	Phe	Val	Gly	Val	Arg	Leu	Cys	Arg	Arg	Ala	Arg	Glu	705	710	715
																		720

Ala Ser Leu Gly Asp Tyr Ser Val Pro Glu Gly His Phe Pro Ser His
725 730 735

Leu Val Asp Val Ser Gly Ala Gly Thr Leu Ser Gln Ser Tyr Gln Tyr
740 745 750

Glu Val Cys Leu Asn Gly Gly Thr Arg Thr Asn Glu Phe Asn Phe Leu
755 760 765

Lys Pro Leu Phe Pro Ile Leu Pro Thr Gln Ala Ala Ala Ala Glu Glu
770 775 780

Arg Glu Asn Ala Val Val His Asn Ser Val Gly Phe Tyr
785 790 795

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAAACACGGG GGAAATGACA GTAGCAAAGA ATCTGGACTA TGAAGAATGC TCATTGTATG	60
AAATGGAAAT ACAGGCTGAA GATGTGGGGG CGCTTCTGGG GAGGAGCAAA GTGGTAATTA	120
TGGTAGAAGA TGTAATGAC AATCGGCCAG AAGTGACCAT TACATCCTTG TTTAACCCGG	180
TATTGGAAAA TTCTCTTCCC GGGACAGTAA TTGCCTTCTT GAATGTGCAT GACCGAGACT	240
CTGGAAAGAA CGGCCAAGTT GTCTGTTACA CGCATGATAA CTTACCTTTT AAATTAGAAA	300
AGTCAATAGA TAATTATTAT AGATTGGTGA CATGGAAATA TTTGGACCGA GAAAAAGTCT	360
CCATCTACAA TATCACAGTG ATAGCCTCAG ATCTAGGAGC CCACTCTGTC ACTGAAACTT	420
ACATTGCCCT GATTGTGGCA GACACTAATG ACAACCCTCC TCGTTTTCCT CACACCTCCT	480
ACACAGCCTA TATTCCAGAG AACAACCTGA GGGGCGCCTC CATCTTCTCA CTGACTGCAC	540
ATGATCCTGA CAGTCAGGAA AATGCACAGG TCACTTACTC TGTGTCTGAG GACACCATAC	600
AGGGAGTGCC TTTGTCCTCT TATATCTCCA TCAACTCAGA TACTGGTGTC CTGTATGCAC	660
TGCACTCTTT TGACTTCGAG AAGATACAAG ACTTGCAGCT ACTGGTTGTT GCCACTGACA	720
GTGGAAGCCC ACCTCTCAGC AGCAATGTGT CATTGAGCTT GTTTGTGTTG GACCAGAACG	780
ACAACGCACC TGAGATTCTA TATCCTAGCT TCCCCACAGA TGGCTCCACT GGTGTGGAAC	840
TAGCACCCCG CTCTGCAGAG CCTGGATACC TAGTGACCAA AGTGGTGGCA GTGGACAAAG	900
ACTCAGGACA GAATGCTTGG CTGTCCTACC GTCTGCTGAA GGCCAGCGAA CCTGGGCTCT	960
TCTCTGTAGG ACTTCACACG GGTGAGGTGC GTACAGCGAG GGCCCTGCTG GACAGAGATG	1020

CTCTCAAACA GAATCTGGTG ATGGCCGTGC AGGACCATGG CCAACCCCCT CTCTCGGCCA	1080
CTGTA ACTCT CACTGTGGCA GTGGCTAACA GCATCCCTGA GGTGTTGGCT GACTTGAGCA	1140
GCATTAGGAC CCCTGGGGTA CCAGAGGATT CTGATATCAC GCTCCACCTG GTGGTGGCAG	1200
TGGCTGTGGT CTCCTGTGTC TTCCTTGTCT TTGTCATTGT CCTCCTAGCT CTCAGGCTTC	1260
AGCGCTGGCA GAAGTCTCGC CAGCTCCAGG GCTCCAAAGG TGGATTGGCT CCTGCACCTC	1320
CATCACATTT TGTGGGCATC GACGGGGTAC AGGCTTTTCT ACAAACCTAT TCTCATGAAG	1380
TCTCGCTCAC TTCAGGCTCC CAGACAAGCC ACATTATCTT TCCTCAGCCC AACTATGCAG	1440
ACATGCTCAT TAACCAAGAA GGCTGTGAGA AAAATGATTC CTTATTAACA TCCATAGATT	1500
TTCATGAGAG TAACCGTGAA GATGCTTGCG CCCC GCAAGC CCCGCCAAC ACTGACTGGC	1560
GTTTCTCTCA AGCCCAGAGA CCCGGCACGA GCGGATCCCA AAATGGGGAT GAAACCGGCA	1620
CCTGGCCCAA CAACCAGTTC GATACAGAGA TGCTGCAAGC CATGATCTTG GCCTCTGCCA	1680
GTGAAGCCGC TGATGGGAGC TCCACTCTGG GAGGGGGCAC TGGCACTATG GGTTTGAGCG	1740
CTCGATATGG ACCCCAGTTT ACCCTGCAGC ACGTGCCTGA CTACCGCCAG AACGTGTACA	1800
TCCCTGGCAG CAATGCCACA CTGACCAACG CAGCTGGCAA ACGAGATGGC AAGGCTCCGG	1860
CAGGCGGCAA TGGCAACAAC AACAAGTCGG GCAAGAAAGA GAAGAAGTAA TATGGAGGCC	1920
AGGCCTTGAG CCACAGGGCA GCCTCCCTCC CCAGCCAGTC CAGCTTGTC TTA CTGTAC	1980
CCAGGCCTCA GAATTTTCAGG GCTCACCCCA GGATTCTGGT AGGAGCCACA GCCAGGCCAT	2040
GCTCCCCGTT GGGAAACAGA AACAAGTGCC CAAGCCAACA CCCCCTCTTT GTACCCTAGG	2100
GGGGTTGAAT ATGCAAAGAG AGTTCTGCTG GGACCCCTA TCCAATCAGT GATTGTACCC	2160
ACATAGGTAG CAGGGTTAGT GTGGATACAC ACACACACAC ACACACACAC ACACACACAA	2220
CCCTTGTCTT CCGCAGTGCC TGCCACTTTC TGGGACTTTC TCATCCCCCT ACGCCCTTCC	2280
TTTATCCTCT CCCACCCAGA CACAGCTGCT GGAGAATAAA TTTGGGGATG CTGATGCTAA	2340
AAAAAAA	2347

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

A GAG GCT GCT CAC CAC CTG GTC CTC ACG GCC TCG GAT GGC GGC AAG	46
Glu Ala Ala His His Leu Val Leu Thr Ala Ser Asp Gly Gly Lys	
1 5 10 15	
CCG CCT CGC TCT AGC ACA GTG CGC ATC CAC GTG ACA GTG TTG GAT ACA	94
Pro Pro Arg Ser Ser Thr Val Arg Ile His Val Thr Val Leu Asp Thr	
20 25 30	
AAT GAC AAT GCC CCG GTT TTT CCT CAC CCG ATT TAC CGA GTG AAA GTC	142
Asn Asp Asn Ala Pro Val Phe Pro His Pro Ile Tyr Arg Val Lys Val	
35 40 45	
CTT GAG AAC ATG CCC CCA GGC ACG CGG CTG CTT ACT GTA ACA GCC AGC	190
Leu Glu Asn Met Pro Pro Gly Thr Arg Leu Leu Thr Val Thr Ala Ser	
50 55 60	
GAC CCG GAT GAG GGA ATC AAC GGA AAA GTG GCA TAC AAA TTC CGG AAA	238
Asp Pro Asp Glu Gly Ile Asn Gly Lys Val Ala Tyr Lys Phe Arg Lys	
65 70 75	
ATT AAT GAA AAA CAA ACT CCG TTA TTC CAG CTT AAT GAA AAT ACT GGG	286
Ile Asn Glu Lys Gln Thr Pro Leu Phe Gln Leu Asn Glu Asn Thr Gly	
80 85 90 95	
GAA ATA TCA ATA GCA AAA AGT CTA GAT TAT GAA GAA TGT TCA TTT TAT	334
Glu Ile Ser Ile Ala Lys Ser Leu Asp Tyr Glu Glu Cys Ser Phe Tyr	
100 105 110	
GAA ATG GAA ATA CAA GCC GAA GAT GTG GGG GCA CTT CTG GGG AGG ACC	382
Glu Met Glu Ile Gln Ala Glu Asp Val Gly Ala Leu Leu Gly Arg Thr	
115 120 125	
AAA TTG CTC ATT TCT GTG GAA GAT GTA AAT GAC AAT AGA CCA GAA GTG	430
Lys Leu Leu Ile Ser Val Glu Asp Val Asn Asp Asn Arg Pro Glu Val	
130 135 140	
ATC ATT ACG TCT TTG TTT AGC CCA GTG TTA GAA AAT TCT CTT CCC GGG	478
Ile Ile Thr Ser Leu Phe Ser Pro Val Leu Glu Asn Ser Leu Pro Gly	
145 150 155	
ACA GTA ATT GCC TTC TTG AGT GTG CAT GAC CAA GAC TCT GGA AAG AAT	526
Thr Val Ile Ala Phe Leu Ser Val His Asp Gln Asp Ser Gly Lys Asn	
160 165 170 175	
GGT CAA GTT GTC TGT TAC ACA CGT GAT AAT TTA CCT TTT AAA TTA GAA	574
Gly Gln Val Val Cys Tyr Thr Arg Asp Asn Leu Pro Phe Lys Leu Glu	
180 185 190	
AAG TCA ATA GGT AAT TAT TAT AGA TTA GTG ACA AGG AAA TAT TTG GAC	622
Lys Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp	
195 200 205	
CGA GAA AAT GTC TCT ATC TAC AAT ATC ACA GTG ATG GCC TCA GAT CTA	670
Arg Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu	
210 215 220	
GGA ACA CCA CCT CTG TCC ACT GAA ACT CAA ATC GCT CTG CAC GTG GCA	718
Gly Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala	
225 230 235	

GAC Asp 240	ATT Ile	AAC Asn	GAC Asp	AAC Asn	CCT Pro	CCT Pro	ACT Thr	TTC Phe	CCT Pro	CAT His	GCC Ala	TCC Ser	TAC Tyr	TCA Ser	GCG Ala 255	766
TAT Tyr	ATC Ile	CTA Leu	GAG Glu	AAC Asn 260	AAC Asn	CTG Leu	AGA Arg	GGA Gly	GCC Ala 265	TCC Ser	ATC Ile	TTT Phe	TCC Ser	TTG Leu 270	ACT Thr	814
GCA Ala	CAC His	GAC Asp	CCC Pro 275	GAC Asp	AGC Ser	CAG Gln	GAG Glu	AAT Asn 280	GCC Ala	CAG Gln	GTC Val	ACT Thr	TAC Tyr	TCT Ser	GTG Val	862
ACC Thr	GAG Glu	GAC Asp 290	ACG Thr	CTG Leu	CAG Gln	GGG Gly	GCG Ala 295	CCC Pro	CTG Leu	TCC Ser	TCG Ser	TAT Tyr 300	ATC Ile	TCC Ser	ATC Ile	910
AAC Asn 305	TCT Ser	GAC Asp	ACC Thr	GGT Gly	GTC Val	CTG Leu 310	TAT Tyr	GCG Ala	CTG Leu	CAA Gln	TCT Ser 315	TTT Phe	GAC Asp	TAT Tyr	GAG Glu	958
CAG Gln 320	ATC Ile	CGA Arg	GAC Asp	CTG Leu	CAG Gln 325	CTA Leu	CTG Leu	GTA Val	ACA Thr	GCC Ala 330	AGC Ser	GAC Asp	AGC Ser	GGG Gly	GAC Asp 335	1006
CCG Pro	CCC Pro	CTC Leu	AGC Ser	AGC Ser 340	AAC Asn	ATG Met	TCA Ser	CTG Leu	AGC Ser 345	CTG Leu	TTC Phe	GTG Val	CTG Leu	GAC Asp 350	CAG Gln	1054
AAT Asn	GAC Asp	AAC Asn 355	GCG Ala	CCC Pro	GAG Glu	ATC Ile	CTG Leu	TAC Tyr 360	CCC Pro	GCC Ala	CTC Leu	CCC Pro	ACA Thr 365	GAC Asp	GGT Gly	1102
TCC Ser	ACT Thr	GGC Gly 370	GTG Val	GAG Glu	CTG Leu	GCG Ala	CCC Pro 375	CGC Arg	TCC Ser	GCA Ala	GAG Glu	CGT Arg 380	GGC Gly	TAC Tyr	CTG Leu	1150
GTG Val	ACC Thr 385	AAG Lys	GTG Val	GTG Val	GCG Ala	GTG Val 390	GAC Asp	AGA Arg	GAC Asp	TCG Ser	GGC Gly 395	CAG Gln	AAC Asn	GCC Ala	TGG Trp	1198
CTG Leu 400	TCC Ser	TAC Tyr	CGC Arg	CTG Leu	CTC Leu 405	AAG Lys	GCC Ala	AGC Ser	GAG Glu	CCG Pro 410	GGA Gly	CTC Leu	TTC Phe	TCG Ser	GTG Val 415	1246
GGT Gly	CTG Leu	CAC His	ACG Thr	GGC Gly 420	GAG Glu	GTG Val	CGC Arg	ACG Thr	GCG Ala 425	CGA Arg	GCC Ala	CTG Leu	CTG Leu	GAC Asp 430	AGA Arg	1294
GAC Asp	GCG Ala	CTC Leu	AAG Lys 435	CAG Gln	AGC Ser	CTC Leu	GTG Val	GTG Val 440	GCC Ala	GTC Val	CAG Gln	GAC Asp	CAT His 445	GGC Gly	CAG Gln	1342
CCC Pro	CCT Pro	CTC Leu 450	TCC Ser	GCC Ala	ACT Thr	GTC Val	ACG Thr 455	CTC Leu	ACC Thr	GTA Val	GCC Ala	GTG Val 460	GCT Ala	GAC Asp	AGC Ser	1390
ATC Ile 465	CCC Pro	GAA Glu	GTC Val	CTG Leu	ACC Thr	GAG Glu 470	TTG Leu	GGC Gly	AGT Ser	CTG Leu	AAG Lys 475	CCT Pro	TCG Ser	GTC Val	GAC Asp	1438

CCG AAC GAT TCG AGC CTT ACA CTC TAT CTC GTG GTG GCA GTG GCT GCC	1486
Pro Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala	
480 485 490 495	
ATC TCC TGT GTC TTC CTC GCC TTT GTC GCT GTG CTT CTG GGG CTC AGG	1534
Ile Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg	
500 505 510	
CTG AGG CGC TGG CAC AAG TCA CGC CTG CTC CAG GAT TCC GGT GGC AGA	1582
Leu Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg	
515 520 525	
TTG GTA GGC GTG CCT GCC TCA CAT TTT GTG GGT GTT GAG GAG GTA CAG	1630
Leu Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Glu Val Gln	
530 535 540	
GCT TTC CTG CAG ACC TAT TCC CAG GAA GTC TCC CTC ACC GCC GAC TCG	1678
Ala Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser	
545 550 555	
CGG AAG AGT CAC CTG ATC TTT CCC CAG CCC AAC TAC GCA GAC ATG CTC	1726
Arg Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu	
560 565 570 575	
ATC AGT CAG GAG GGC TGT GAG AAA AAT GAT TCT TTG TTA ACA TCC GTA	1774
Ile Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val	
580 585 590	
GAT TTT CAT GAA TAT AAG AAT GAA GCT GAT CAT GGT CAG GTG AGT TTA	1822
Asp Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu	
595 600 605	
GTT CTT TGC TTG CTT TTA ATT TCC AGA TGAATTTTAT TTGGCATAAA	1869
Val Leu Cys Leu Leu Leu Ile Ser Arg	
610 615	
TTATGTTTTG AAAACATTG TGAAGATAGT TGAAAATAAT TTTTAAGGTG TATCACAGAG	1929
TTTTGGGTTT ATTTTGGTGG TGTTACCAAA AAATTGAACT CTAATAGTCA TAGGTTATTG	1989
TTTCATTTGC TTTTAAACGA CTTGGAAAAG ATTGTTCCAC CATTTTAAAC CTTCCAGTAT	2049
TTTATTCCTA TTATCACTCA TTCACTTAAG AAGTAGCTAC CCGTCCATAC TGGTAATTTT	2109
GCTATTGTTT GTTTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTAT CCCAACTAG	2169
AACTTCAGAA AATTATCAAG AAGTCTAAAG CCTTGTTATT AGCTTAGCAA AAGTAAAATA	2229
TATCTCAGAA TTTTATAGGT TATGTTTAGC ATTTGAACCT GTAAGTAGGC TCTTGATAT	2289
TTCTTCACTT TAAACCTCTT TTCTGAGCCC TGTTTCTGTA CCAGTGCCCT TCAAACTTT	2349
AATACTTCTT ACCATCCTTC AAAACATGAA CAAACTTTAA AGATGGATCT TGGTGGGAGA	2409
TGAGACTGGT TACTAAATAT TAAGTATGTG AGTCAGTGGT CACCTGGGCT CCATCCCCAT	2469
GGAGACATGA AATCTAAAGC CTAGAATGTC CATTGCTCCC CCAAACAAA AACAAAAGCA	2529
AAAACATTAG ATCTGAATTA AAATGTAATT TTAACTGTT GAAAGTGACT TTTGTAAAT	2589
ATGTAAGAAC ATATTTCAAT ACAATTCCAA TTAGCTGTTT CGGTTGTGCA TTGATGTGAA	2649

GTGGTGAGAA TGTTGATATT AAGAACCAAT GTTTCAGGTA CACAAGTTCT AAATAAGCTG	2709
ATCAATTCAA TTAAAGTTAT TCACTCTTGG CTGGACACAG TGCCTCATGT CTGAAATCCC	2769
AGCACTTTGG GAGGCTGGGG CAGGAGGACC GCTTGAGCCC CGGGGGTTTG AAACCTGCAGT	2829
GAGCTATGAT CATGCCACTG CACTCCAGCC TAGGTGGCAG AACTAGACCC TGTCTCTAAA	2889
AAACTATTA TTAGGCCGCG TCGGGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGAC	2949
TGAGGTGGGT GGATCACCTG AGC	2972

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Glu	Ala	Ala	His	His	Leu	Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Lys	Pro	1	5	10	15
Pro	Arg	Ser	Ser	Thr	Val	Arg	Ile	His	Val	Thr	Val	Leu	Asp	Thr	Asn	20	25	30	
Asp	Asn	Ala	Pro	Val	Phe	Pro	His	Pro	Ile	Tyr	Arg	Val	Lys	Val	Leu	35	40	45	
Glu	Asn	Met	Pro	Pro	Gly	Thr	Arg	Leu	Leu	Thr	Val	Thr	Ala	Ser	Asp	50	55	60	
Pro	Asp	Glu	Gly	Ile	Asn	Gly	Lys	Val	Ala	Tyr	Lys	Phe	Arg	Lys	Ile	65	70	75	80
Asn	Glu	Lys	Gln	Thr	Pro	Leu	Phe	Gln	Leu	Asn	Glu	Asn	Thr	Gly	Glu	85	90	95	
Ile	Ser	Ile	Ala	Lys	Ser	Leu	Asp	Tyr	Glu	Glu	Cys	Ser	Phe	Tyr	Glu	100	105	110	
Met	Glu	Ile	Gln	Ala	Glu	Asp	Val	Gly	Ala	Leu	Leu	Gly	Arg	Thr	Lys	115	120	125	
Leu	Leu	Ile	Ser	Val	Glu	Asp	Val	Asn	Asp	Asn	Arg	Pro	Glu	Val	Ile	130	135	140	
Ile	Thr	Ser	Leu	Phe	Ser	Pro	Val	Leu	Glu	Asn	Ser	Leu	Pro	Gly	Thr	145	150	155	160
Val	Ile	Ala	Phe	Leu	Ser	Val	His	Asp	Gln	Asp	Ser	Gly	Lys	Asn	Gly	165	170	175	
Gln	Val	Val	Cys	Tyr	Thr	Arg	Asp	Asn	Leu	Pro	Phe	Lys	Leu	Glu	Lys	180	185	190	

Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp Arg
195 200 205

Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu Gly
210 215 220

Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala Asp
225 230 235 240

Ile Asn Asp Asn Pro Pro Thr Phe Pro His Ala Ser Tyr Ser Ala Tyr
245 250 255

Ile Leu Glu Asn Asn Leu Arg Gly Ala Ser Ile Phe Ser Leu Thr Ala
260 265 270

His Asp Pro Asp Ser Gln Glu Asn Ala Gln Val Thr Tyr Ser Val Thr
275 280 285

Glu Asp Thr Leu Gln Gly Ala Pro Leu Ser Ser Tyr Ile Ser Ile Asn
290 295 300

Ser Asp Thr Gly Val Leu Tyr Ala Leu Gln Ser Phe Asp Tyr Glu Gln
305 310 315 320

Ile Arg Asp Leu Gln Leu Leu Val Thr Ala Ser Asp Ser Gly Asp Pro
325 330 335

Pro Leu Ser Ser Asn Met Ser Leu Ser Leu Phe Val Leu Asp Gln Asn
340 345 350

Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp Gly Ser
355 360 365

Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Arg Gly Tyr Leu Val
370 375 380

Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu
385 390 395 400

Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly Leu Phe Ser Val Gly
405 410 415

Leu His Thr Gly Glu Val Arg Thr Ala Arg Ala Leu Leu Asp Arg Asp
420 425 430

Ala Leu Lys Gln Ser Leu Val Val Ala Val Gln Asp His Gly Gln Pro
435 440 445

Pro Leu Ser Ala Thr Val Thr Leu Thr Val Ala Val Ala Asp Ser Ile
450 455 460

Pro Glu Val Leu Thr Glu Leu Gly Ser Leu Lys Pro Ser Val Asp Pro
465 470 475 480

Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala Ile
485 490 495

Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg Leu
500 505 510

Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg Leu
515 520 525

Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Glu Val Gln Ala
530 535 540

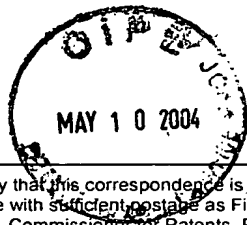
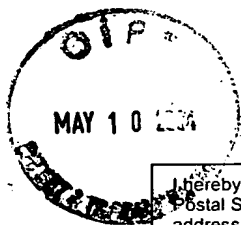
Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser Arg
545 550 555 560

Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Ile
565 570 575

Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val Asp
580 585 590

Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu Val
595 600 605

Leu Cys Leu Leu Leu Ile Ser Arg
610 615



I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as First Class Mail, in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on the date shown below.

Dated: 5-7-04

Signature: Katherine L. Neville

Katherine L. Neville, Ph.D.

Docket No.: 27866/37501
(PATENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re , Application of: Suzuki, S.

Application No.: 09/880,573

Group Art Unit: 1647

Filed: June 13, 2001

Examiner: David Romeo

For: Protocadherin Materials and Methods

STATEMENT UNDER 37 C.F.R. §1.821

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821 and 1.825, are the same and include no new matter.

May 7, 2004

Respectfully submitted,

MARSHALL, GERSTEIN & BORUN LLP
6300 Sears Tower
233 South Wacker Drive
Chicago, Illinois 60606-6357
(312) 474-6300

By: Katherine L. Neville

Katherine L. Neville, Ph.D.

Reg. No. 53,379

Agent for Applicants



PC43	EC 1	(29)	ASTVIHVEIPEEREK-----GFAVGNVUANL---GLDLGSLSA--	(63)
	EC 2	(136)	PTQEMKLEISEAVAP-----GTRFPLESAH---DPDLGSNSL--	(169)
	EC 3	(245)	NQSLYRARVPGGCTS-----GTRVQVQLAT---DLDEGPNGE--	(278)
	EC 4	(353)	TVTSVYSPVPEDAS-----GTVIALLSVT---DLDAGENGL--	(385)
	EC 5	(457)	SOSSYDVYIEENNLP-----GAPILNLSVW---DPDAPQONAR--	(490)
	EC 6	(567)	LYPRPGSSVEMLPRTSA-GHLVSRVVGW----DADAGHNAW--	(604)
PC42	EC 1	(42)	VPEEQPNTLI-----GSL-----AADYGFPDVG--	(65)
	EC 2	(147)	ASPVITTLAIPENTNI-----GSLFPIPLAS---DRDAGPNGV--	(180)
	EC 3	(247)	ERPSYEAELSENSPI-----GHSVIOVKAN---DSDQGANAEE--	(280)
	EC 4	(354)	EIRGIGLVTHODGMANISEDVAETAVALVQVSDRDEGENAA--	(395)
	EC 5	(473)	TQSVTEVAFPENKPP-----GEVIAEITAS---DADSGSNAE--	(506)
	EC 6	(579)	MLSGYNFSVMENMPA-----LSPVGMVTVI---DGDKGENAQ--	(612)
	EC 7	(682)	TAPSNNTSHKLLTPQTRL---GETVSQVAEE---DFDSGVNAE--	(717)
FAT	EC18	(1)	EDTVYSFDIPENAOQR-----GYQVGQIVAR---DADLGQNAQ--	(34)
N-CAD	EC 1	(1)	DWVIPPINLPENSRG-----PFPQELVRIRS---DRDKNLSLRYT	(37)
	EC 2	(109)	LHQVWNGSVPEGSKP-----GTVYMTVTAI---DADDPNALNGM	(144)
	EC 3	(224)	TAMTFYGEVPEENRVD-----IIVANLTVT---DKDQHPHTPAWN	(258)
	EC 4	(339)	APNPKIIRQEEGLHA-----GTMLTTFTAG---DPDRYMQQN--	(372)
	EC 5	(447)	LPQEAETCETDPNSINITAL-----DYDIDPNAGP--	(478)

****0***v*EN***-----GT*v**v*A*-----D*D*G*N*-----

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FIGURE 1A



PC43	EC 1	(64)	RRFPVVGASRR-----FFEVRNRET-----GEMFVNR-----	(91)
	EC 2	(170)	QTYELSRNEY-----FALRVQTRDSTKYAELVLERA---	(201)
	EC 3	(279)	IIYSFGSHNRAGVRQL--FALDLVT-----GMLTIKGR----	(309)
	EC 4	(386)	VTCEVPPGLP-----FSLTSSLKNYFTLKTSAD-----	(413)
	EC 5	(491)	LSFFLLEQGAETGLVGRYFTINRDN-----GIVSSLVP----	(523)
	EC 6	(605)	LSYSLFGSPNOSL-----FAIGLHT-----GQISTARPV---	(633)
PC42	EC 1	(66)	HLYKLEVGAPE-----YLRVDGKT-----GDIFTTETS---	(92)
	EC 2	(181)	ASYELQVAED-----QEEKQPQLIVMGN-----	(203)
	EC 3	(281)	IEYTFHOAPEVVRRL---LRLDRNT-----GLITVQGP-----	(310)
	EC 4	(396)	VTCVVAGDVP-----FOLROASETGSDSKKYFLOTTTP	(429)
	EC 5	(507)	LVYSLEPEPAKGL-----FTISPET-----GEIQVKT-----	(535)
	EC 6	(613)	VQLSVEODNGD-----FVIONGT-----GTILSSLS-----	(638)
	EC 7	(718)	LIYSIAGGNPYGL-----FOIGSHS-----GAITLEKE-----	(745)
FAT	EC18	(35)	LSYGVVSDWANDV-----FSLNPOT-----GMLTLTAR----	(62)
N-CAD	EC 1	(38)	VTGPGADQPPTGI-----FIINPIS-----GQLSVTKP-----	(65)
	EC 2	(145)	LRYRILSOAPSTSPNM-FINNNET-----GDIITVAAG----	(177)
	EC 3	(259)	AVTRISGGDPTGR-----FAIQTDPNND--GLVTVVKP-----	(290)
	EC 4	(373)	IRYTKLSDPAN-----WLKIDPVN-----GOITTIIV-----	(399)
	EC 5	(479)	FAYDLPLSPVTIKRN---WTITRLN-----GDFAQLNLK----	(509)

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FIGURE 1B

PC43
 EC 1 (92) LDREELCGTLPSCVTLELVENP-----LELFSVEVVIODINDNNPAF (135)
 EC 2 (202) LDREREPSLQLVLTALDGGTPAL-----SASLP IHIKVL DANDNAPVF (244)
 EC 3 (310) LDFEDTKLHEIYIOAKDGANPE-----GAHCKVLVEVVDVNDNAPEI (352)
 EC 4 (414) LDRETVPEYNLSITARDAGTPSL-----SALTIVRVQVSDINDNPPQS (456)
 EC 5 (524) LDYEDRRREFELTAHISDGGTPVL-----ATNISVNI FVTD RNDNAPQV (566)
 EC 6 (634) ODTDSPRQTLTVL-IKDNGEPSLTTATLTVSVTEDSPEARAEFSGSAPREQKN (688)

PC42
 EC 1 (93) IDREGLRECONQLPGDPCILEFEVSITDLVONAS--PRLLEGQIEVODINDNTPNF (146)
 EC 2 (204) LDRERWDSYDLTIKVODGGSPPR-----ATSALLRVTVLDTNDNAPKF (246)
 EC 3 (311) VDREDLSTLRFSLAKDRGTPK-----SARQVVTVKMDNDNAPTI (353)
 EC 4 (430) LDYEKVKDYTIEIVAVDSGNPPL-----SSTNSLKQVVDVNDNAPVF (472)
 EC 5 (536) LDREQRESYELKVVAADRGSPL-----QGTATVLVNVLDCNDNDPKF (578)
 EC 6 (639) FDREQQSTYTFQLKAVDGGVPPR-----SAYVGTINVL DENDNAPYI (681)
 EC 7 (746) IERRHGLHRLVVKVSDRGKPPRYGTALVHLYVNETLANRTLLETLLGHSLDTPLD (801)
 (802) IDIAGDPEYERSKQRGN (818)

FAT
 EC18 (63) LDYEEVQHYIILVQAO DNGQPSL-----STTITVYCNVLDLNDNAPIF (105)

N-CAD
 EC 1 (66) LDREQIARFHLRAHAVDINGNQV-----ENPIDIVINVIDMNDNRPEF (108)
 EC 2 (178) LDREKVQQYTLIIQATDMEGNPTYGL-----SNTATAVITVTDVNDNPPEF (223)
 EC 3 (291) IDFETNRMFVLTVAAENQVPLAKGIOHPP-----QSTATSVTVTDVNE-NPYF (338)
 EC 4 (400) LDRESPNVKNNIYNATFLASDNGIPPM-----SGTGLQIYLLDINDNAPQV (446)
 EC 5 (510) IKFLEAGIYEVPIIITDSGNPPKSNKS-----ILRVRCQCFNGDCTDVDR (557)

MOTIF
 LDRE****O*L*v*A*D*G*P**-----**T*TV*v*v*D*NDNAP*F

FIGURE 1C